SEQUENCE LISTING

<110> INSTITUT PASTEUR
      CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE
      UNIVERSITE PARIS 7
      VAN DER WERF, Sylvie
      ESCRIOU, Nicolas
      CRESCENZO-CHAIGNE, Bernadette
      MANUGUERRA, Jean-Claude
      KUNST, Franck
      CALLENDRET, Benoît
      BETTON, Jean-Michel
      LORIN, Valérie
      GERBAUD, Sylvie
      BURGUIERE, Ana Maria
      AZEBI, Saliha
      CHARNEAU, Pierre
      TANGY, Frédéric
      COMBREDET, Chantal
      DELAGNEAU, Jean-François
      MARTIN, Monique

<120> NOVEL STRAIN OF SARS-ASSOCIATED CORONAVIRUS AND APPLICATIONS THEREOF.

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                              Met Phe Ile Phe Leu Leu Phe Leu
                               1               5
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Thr Leu Thr Ser Gly Ser Asp Leu Asp Arg Cys Thr Thr Phe Asp Asp
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Val Gln Ala Pro Asn Tyr Thr Gln His Thr Ser Ser Met Arg Gly Val
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Tyr Tyr Pro Asp Glu Ile Phe Arg Ser Asp Thr Leu Tyr Leu Thr Gln
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gat tta ttt ctt cca ttt tat tct aat gtt aca ggg ttt cat act att      304
Asp Leu Phe Leu Pro Phe Tyr Ser Asn Val Thr Gly Phe His Thr Ile
                60                  65                  70

aat cat acg ttt ggc aac cct gtc ata cct ttt aag gat ggt att tat      352
Asn His Thr Phe Gly Asn Pro Val Ile Pro Phe Lys Asp Gly Ile Tyr
            75                  80                  85

ttt gct gcc aca gag aaa tca aat gtt gtc cgt ggt tgg gtt ttt ggt      400
Phe Ala Ala Thr Glu Lys Ser Asn Val Val Arg Gly Trp Val Phe Gly
        90                  95                  100

tct acc atg aac aac aag tca cag tcg gtg att att att aac aat tct      448
Ser Thr Met Asn Asn Lys Ser Gln Ser Val Ile Ile Ile Asn Asn Ser
105                 110                 115                 120

act aat gtt gtt ata cga gca tgt aac ttt gaa ttg tgt gac aac cct      496
Thr Asn Val Val Ile Arg Ala Cys Asn Phe Glu Leu Cys Asp Asn Pro
                125                 130                 135

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Phe Phe Ala Val Ser Lys Pro Met Gly Thr Gln Thr His Thr Met Ile
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Phe Asp Asn Ala Phe Asn Cys Thr Phe Glu Tyr Ile Ser Asp Ala Phe
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tcg ctt gat gtt tca gaa aag tca ggt aat ttt aaa cac tta cga gag      640
Ser Leu Asp Val Ser Glu Lys Ser Gly Asn Phe Lys His Leu Arg Glu
        170                 175                 180

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Phe Val Phe Lys Asn Lys Asp Gly Phe Leu Tyr Val Tyr Lys Gly Tyr
185                 190                 195                 200

caa cct ata gat gta gtt cgt gat cta cct tct ggt ttt aac act ttg      736
Gln Pro Ile Asp Val Val Arg Asp Leu Pro Ser Gly Phe Asn Thr Leu
                205                 210                 215

aaa cct att ttt aag ttg cct ctt ggt att aac att aca aat ttt aga      784
Lys Pro Ile Phe Lys Leu Pro Leu Gly Ile Asn Ile Thr Asn Phe Arg
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gcc att ctt aca gcc ttt tca cct gct caa gac att tgg ggc acg tca      832
Ala Ile Leu Thr Ala Phe Ser Pro Ala Gln Asp Ile Trp Gly Thr Ser
            235                 240                 245

gct gca gcc tat ttt gtt ggc tat tta aag cca act aca ttt atg ctc      880
Ala Ala Ala Tyr Phe Val Gly Tyr Leu Lys Pro Thr Thr Phe Met Leu
        250                 255                 260

aag tat gat gaa aat ggt aca atc aca gat gct gtt gat tgt tct caa      928
Lys Tyr Asp Glu Asn Gly Thr Ile Thr Asp Ala Val Asp Cys Ser Gln
265                 270                 275                 280

aat cca ctt gct gaa ctc aaa tgc tct gtt aag agc ttt gag att gac      976
Asn Pro Leu Ala Glu Leu Lys Cys Ser Val Lys Ser Phe Glu Ile Asp
                285                 290                 295

aaa gga att tac cag acc tct aat ttc agg gtt gtt ccc tca gga gat     1024
Lys Gly Ile Tyr Gln Thr Ser Asn Phe Arg Val Val Pro Ser Gly Asp
                300                 305                 310

gtt gtg aga ttc cct aat att aca aac ttg tgt cct ttt gga gag gtt     1072
Val Val Arg Phe Pro Asn Ile Thr Asn Leu Cys Pro Phe Gly Glu Val
            315                 320                 325

ttt aat gct act aaa ttc cct tct gtc tat gca tgg gag aga aaa aaa     1120
Phe Asn Ala Thr Lys Phe Pro Ser Val Tyr Ala Trp Glu Arg Lys Lys
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345                 350                 355                 360
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Phe Ser Thr Phe Lys Cys Tyr Gly Val Ser Ala Thr Lys Leu Asn Asp
                365                 370                 375
ctt tgc ttc tcc aat gtc tat gca gat tct ttt gta gtc aag gga gat     1264
Leu Cys Phe Ser Asn Val Tyr Ala Asp Ser Phe Val Val Lys Gly Asp
                380                 385                 390
gat gta aga caa ata gcg cca gga caa act ggt gtt att gct gat tat     1312
Asp Val Arg Gln Ile Ala Pro Gly Gln Thr Gly Val Ile Ala Asp Tyr
                395                 400                 405
aat tat aaa ttg cca gat gat ttc atg ggt tgt gtc ctt gct tgg aat     1360
Asn Tyr Lys Leu Pro Asp Asp Phe Met Gly Cys Val Leu Ala Trp Asn
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act agg aac att gat gct act tca act ggt aat tat aat tat aaa tat     1408
Thr Arg Asn Ile Asp Ala Thr Ser Thr Gly Asn Tyr Asn Tyr Lys Tyr
425                 430                 435                 440
agg tat ctt aga cat ggc aag ctt agg ccc ttt gag aga gac ata tct     1456
Arg Tyr Leu Arg His Gly Lys Leu Arg Pro Phe Glu Arg Asp Ile Ser
                445                 450                 455
aat gtg cct ttc tcc cct gat ggc aaa cct tgc acc cca cct gct ctt     1504
Asn Val Pro Phe Ser Pro Asp Gly Lys Pro Cys Thr Pro Pro Ala Leu
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aat tgt tat tgg cca tta aat gat tat ggt ttt tac acc act act ggc     1552
Asn Cys Tyr Trp Pro Leu Asn Asp Tyr Gly Phe Tyr Thr Thr Thr Gly
            475                 480                 485
att ggc tac caa cct tac aga gtt gta gta ctt tct ttt gaa ctt tta     1600
Ile Gly Tyr Gln Pro Tyr Arg Val Val Val Leu Ser Phe Glu Leu Leu
            490                 495                 500
aat gca ccg gcc acg gtt tgt gga cca aaa tta tcc act gac ctt att     1648
Asn Ala Pro Ala Thr Val Cys Gly Pro Lys Leu Ser Thr Asp Leu Ile
505                 510                 515                 520
aag aac cag tgt gtc aat ttt aat ttt aat gga ctc act ggt act ggt     1696
Lys Asn Gln Cys Val Asn Phe Asn Phe Asn Gly Leu Thr Gly Thr Gly
                525                 530                 535
gtg tta act cct tct tca aag aga ttt caa cca ttt caa caa ttt ggc     1744
Val Leu Thr Pro Ser Ser Lys Arg Phe Gln Pro Phe Gln Gln Phe Gly
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cgt gat gtt tct gat ttc act gat tcc gtt cga gat cct aaa aca tct     1792
Arg Asp Val Ser Asp Phe Thr Asp Ser Val Arg Asp Pro Lys Thr Ser
            555                 560                 565
gaa ata tta gac att tca cct tgc tct ttt ggg ggt gta agt gta att     1840
Glu Ile Leu Asp Ile Ser Pro Cys Ser Phe Gly Gly Val Ser Val Ile
            570                 575                 580
aca cct gga aca aat gct tca tct gaa gtt gct gtt cta tat caa gat     1888
Thr Pro Gly Thr Asn Ala Ser Ser Glu Val Ala Val Leu Tyr Gln Asp
585                 590                 595                 600
gtt aac tgc act gat gtt tct aca gca att cat gca gat caa ctc aca     1936
Val Asn Cys Thr Asp Val Ser Thr Ala Ile His Ala Asp Gln Leu Thr
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cca gct tgg cgc ata tat tct act gga aac aat gta ttc cag act caa     1984
Pro Ala Trp Arg Ile Tyr Ser Thr Gly Asn Asn Val Phe Gln Thr Gln
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gca ggc tgt ctt ata gga gct gag cat gtc gac act tct tat gag tgc     2032
Ala Gly Cys Leu Ile Gly Ala Glu His Val Asp Thr Ser Tyr Glu Cys
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Asp Ile Pro Ile Gly Ala Gly Ile Cys Ala Ser Tyr His Thr Val Ser
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665             670             675                 680
tta ggt gct gat agt tca att gct tac tct aat aac acc att gct ata     2176
Leu Gly Ala Asp Ser Ser Ile Ala Tyr Ser Asn Asn Thr Ile Ala Ile
            685             690                 695
cct act aac ttt tca att agc att act aca gaa gta atg cct gtt tct     2224
Pro Thr Asn Phe Ser Ile Ser Ile Thr Thr Glu Val Met Pro Val Ser
            700             705                 710
atg gct aaa acc tcc gta gat tgt aat atg tac atc tgc gga gat tct     2272
Met Ala Lys Thr Ser Val Asp Cys Asn Met Tyr Ile Cys Gly Asp Ser
            715             720                 725
act gaa tgt gct aat ttg ctt ctc caa tat ggt agc ttt tgc aca caa     2320
Thr Glu Cys Ala Asn Leu Leu Leu Gln Tyr Gly Ser Phe Cys Thr Gln
            730             735                 740
cta aat cgt gca ctc tca ggt att gct gct gaa cag gat cgc aac aca     2368
Leu Asn Arg Ala Leu Ser Gly Ile Ala Ala Glu Gln Asp Arg Asn Thr
745             750             755                 760
cgt gaa gtg ttc gct caa gtc aaa caa atg tac aaa acc cca act ttg     2416
Arg Glu Val Phe Ala Gln Val Lys Gln Met Tyr Lys Thr Pro Thr Leu
            765             770                 775
aaa tat ttt ggt ggt ttt aat ttt tca caa ata tta cct gac cct cta     2464
Lys Tyr Phe Gly Gly Phe Asn Phe Ser Gln Ile Leu Pro Asp Pro Leu
            780             785                 790
aag cca act aag agg tct ttt att gag gac ttg ctc ttt aat aag gtg     2512
Lys Pro Thr Lys Arg Ser Phe Ile Glu Asp Leu Leu Phe Asn Lys Val
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aca ctc gct gat gct ggc ttc atg aag caa tat ggc gaa tgc cta ggt     2560
Thr Leu Ala Asp Ala Gly Phe Met Lys Gln Tyr Gly Glu Cys Leu Gly
810             815                 820
gat att aat gct aga gat ctc att tgt gcg cag aag ttc aat gga ctt     2608
Asp Ile Asn Ala Arg Asp Leu Ile Cys Ala Gln Lys Phe Asn Gly Leu
825             830             835                 840
aca gtg ttg cca cct ctg ctc act gat gat atg att gct gcc tac act     2656
Thr Val Leu Pro Pro Leu Leu Thr Asp Asp Met Ile Ala Ala Tyr Thr
            845             850                 855
gct gct cta gtt agt ggt act gcc act gct gga tgg aca ttt ggt gct     2704
Ala Ala Leu Val Ser Gly Thr Ala Thr Ala Gly Trp Thr Phe Gly Ala
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ggc gct gct ctt caa ata cct ttt gct atg caa atg gca tat agg ttc     2752
Gly Ala Ala Leu Gln Ile Pro Phe Ala Met Gln Met Ala Tyr Arg Phe
            875             880                 885
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Asn Gly Ile Gly Val Thr Gln Asn Val Leu Tyr Glu Asn Gln Lys Gln
            890             895                 900
atc gcc aac caa ttt aac aag gcg att agt caa att caa gaa tca ctt     2848
Ile Ala Asn Gln Phe Asn Lys Ala Ile Ser Gln Ile Gln Glu Ser Leu
905             910             915                 920
aca aca aca tca act gca ttg ggc aag ctg caa gac gtt gtt aac cag     2896
Thr Thr Thr Ser Thr Ala Leu Gly Lys Leu Gln Asp Val Val Asn Gln
            925             930                 935
aat gct caa gca tta aac aca ctt gtt aaa caa ctt agc tct aat ttt     2944
Asn Ala Gln Ala Leu Asn Thr Leu Val Lys Gln Leu Ser Ser Asn Phe
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ggt gca att tca agt gtg cta aat gat atc ctt tcg cga ctt gat aaa     2992
Gly Ala Ile Ser Ser Val Leu Asn Asp Ile Leu Ser Arg Leu Asp Lys
            955             960                 965
gtc gag gcg gag gta caa att gac agg tta att aca ggc aga ctt caa     3040
Val Glu Ala Glu Val Gln Ile Asp Arg Leu Ile Thr Gly Arg Leu Gln
970             975                 980
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agg gct tct gct aat ctt gct gct act aaa atg tct gag tgt gtt        3133
Arg Ala Ser Ala Asn Leu Ala Ala Thr Lys Met Ser Glu Cys Val
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ctt gga caa tca aaa aga gtt gac ttt tgt gga aag ggc tac cac        3178
Leu Gly Gln Ser Lys Arg Val Asp Phe Cys Gly Lys Gly Tyr His
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ctt atg tcc ttc cca caa gca gcc ccg cat ggt gtt gtc ttc cta        3223
Leu Met Ser Phe Pro Gln Ala Ala Pro His Gly Val Val Phe Leu
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cat gtc acg tat gtg cca tcc cag gag agg aac ttc acc aca gcg        3268
His Val Thr Tyr Val Pro Ser Gln Glu Arg Asn Phe Thr Thr Ala
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cca gca att tgt cat gaa ggc aaa gca tac ttc cct cgt gaa ggt        3313
Pro Ala Ile Cys His Glu Gly Lys Ala Tyr Phe Pro Arg Glu Gly
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gtt ttt gtg ttt aat ggc act tct tgg ttt att aca cag agg aac        3358
Val Phe Val Phe Asn Gly Thr Ser Trp Phe Ile Thr Gln Arg Asn
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Phe Phe Ser Pro Gln Ile Ile Thr Thr Asp Asn Thr Phe Val Ser
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Gly Asn Cys Asp Val Val Ile Gly Ile Ile Asn Asn Thr Val Tyr
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Asp Pro Leu Gln Pro Glu Leu Asp Ser Phe Lys Glu Glu Leu Asp
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Lys Tyr Phe Lys Asn His Thr Ser Pro Asp Val Asp Leu Gly Asp
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Ile Ser Gly Ile Asn Ala Ser Val Val Asn Ile Gln Lys Glu Ile
                1155            1160            1165

gac cgc ctc aat gag gtc gct aaa aat tta aat gaa tca ctc att        3628
Asp Arg Leu Asn Glu Val Ala Lys Asn Leu Asn Glu Ser Leu Ile
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gac ctt caa gaa ttg gga aaa tat gag caa tat att aaa tgg cct        3673
Asp Leu Gln Glu Leu Gly Lys Tyr Glu Gln Tyr Ile Lys Trp Pro
                1185            1190            1195

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Trp Tyr Val Trp Leu Gly Phe Ile Ala Gly Leu Ile Ala Ile Val
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atg gtt aca atc ttg ctt tgt tgc atg act agt tgt tgc agt tgc        3763
Met Val Thr Ile Leu Leu Cys Cys Met Thr Ser Cys Cys Ser Cys
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ctc aag ggt gca tgc tct tgt ggt tct tgc tgc aag ttt gat gag        3808
Leu Lys Gly Ala Cys Ser Cys Gly Ser Cys Cys Lys Phe Asp Glu
                1230            1235            1240

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Asp Asp Ser Glu Pro Val Leu Lys Gly Val Lys Leu His Tyr Thr
                1245            1250            1255

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His Thr Ser Ser Met Arg Gly Val Tyr Tyr Pro Asp Glu Ile Phe Arg.
        35              40              45
Ser Asp Thr Leu Tyr Leu Thr Gln Asp Leu Phe Leu Pro Phe Tyr Ser
    50              55              60
Asn Val Thr Gly Phe His Thr Ile Asn His Thr Phe Gly Asn Pro Val
65              70              75              80
Ile Pro Phe Lys Asp Gly Ile Tyr Phe Ala Ala Thr Glu Lys Ser Asn
            85              90              95
Val Val Arg Gly Trp Val Phe Gly Ser Thr Met Asn Asn Lys Ser Gln
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Ser Val Ile Ile Ile Asn Asn Ser Thr Asn Val Val Ile Arg Ala Cys
        115             120             125
Asn Phe Glu Leu Cys Asp Asn Pro Phe Phe Ala Val Ser Lys Pro Met
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Gly Thr Gln Thr His Thr Met Ile Phe Asp Asn Ala Phe Asn Cys Thr
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Phe Glu Tyr Ile Ser Asp Ala Phe Ser Leu Asp Val Ser Glu Lys Ser
            165             170             175
Gly Asn Phe Lys His Leu Arg Glu Phe Val Phe Lys Asn Lys Asp Gly
            180             185             190
Phe Leu Tyr Val Tyr Lys Gly Tyr Gln Pro Ile Asp Val Val Arg Asp
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Leu Pro Ser Gly Phe Asn Thr Leu Lys Pro Ile Phe Lys Leu Pro Leu
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Gly Ile Asn Ile Thr Asn Phe Arg Ala Ile Leu Thr Ala Phe Ser Pro
225             230             235             240
Ala Gln Asp Ile Trp Gly Thr Ser Ala Ala Ala Tyr Phe Val Gly Tyr
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Leu Lys Pro Thr Thr Phe Met Leu Lys Tyr Asp Glu Asn Gly Thr Ile
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Thr Asp Ala Val Asp Cys Ser Gln Asn Pro Leu Ala Glu Leu Lys Cys
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Ser Val Lys Ser Phe Glu Ile Asp Lys Gly Ile Tyr Gln Thr Ser Asn
    290             295             300
Phe Arg Val Val Pro Ser Gly Asp Val Val Arg Phe Pro Asn Ile Thr
305             310             315             320
Asn Leu Cys Pro Phe Gly Glu Val Phe Asn Ala Thr Lys Phe Pro Ser
            325             330             335
Val Tyr Ala Trp Glu Arg Lys Lys Ile Ser Asn Cys Val Ala Asp Tyr
            340             345             350
Ser Val Leu Tyr Asn Ser Thr Phe Phe Ser Thr Phe Lys Cys Tyr Gly
    355             360             365
Val Ser Ala Thr Lys Leu Asn Asp Leu Cys Phe Ser Asn Val Tyr Ala
    370             375             380
Asp Ser Phe Val Val Lys Gly Asp Asp Val Arg Gln Ile Ala Pro Gly
385             390             395             400
Gln Thr Gly Val Ile Ala Asp Tyr Asn Tyr Lys Leu Pro Asp Asp Phe
            405             410             415
Met Gly Cys Val Leu Ala Trp Asn Thr Arg Asn Ile Asp Ala Thr Ser
            420             425             430
Thr Gly Asn Tyr Asn Tyr Lys Tyr Arg Tyr Leu Arg His Gly Lys Leu
            435             440             445
Arg Pro Phe Glu Arg Asp Ile Ser Asn Val Pro Phe Ser Pro Asp Gly
    450             455             460
Lys Pro Cys Thr Pro Pro Ala Leu Asn Cys Tyr Trp Pro Leu Asn Asp
465             470             475             480
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Tyr Gly Phe Tyr Thr Thr Thr Gly Ile Gly Tyr Gln Pro Tyr Arg Val
            485                     490                 495
Val Val Leu Ser Phe Glu Leu Leu Asn Ala Pro Ala Thr Val Cys Gly
            500                 505                 510
Pro Lys Leu Ser Thr Asp Leu Ile Lys Asn Gln Cys Val Asn Phe Asn
            515             520             525
Phe Asn Gly Leu Thr Gly Thr Gly Val Leu Thr Pro Ser Ser Lys Arg
        530             535             540
Phe Gln Pro Phe Gln Gln Phe Gly Arg Asp Val Ser Asp Phe Thr Asp
    545             550             555             560
Ser Val Arg Asp Pro Lys Thr Ser Glu Ile Leu Asp Ile Ser Pro Cys
                565             570             575
Ser Phe Gly Gly Val Ser Val Ile Thr Pro Gly Thr Asn Ala Ser Ser
            580             585             590
Glu Val Ala Val Leu Tyr Gln Asp Val Asn Cys Thr Asp Val Ser Thr
        595             600             605
Ala Ile His Ala Asp Gln Leu Thr Pro Ala Trp Arg Ile Tyr Ser Thr
    610             615             620
Gly Asn Asn Val Phe Gln Thr Gln Ala Gly Cys Leu Ile Gly Ala Glu
625             630             635             640
His Val Asp Thr Ser Tyr Glu Cys Asp Ile Pro Ile Gly Ala Gly Ile
            645             650             655
Cys Ala Ser Tyr His Thr Val Ser Leu Leu Arg Ser Thr Ser Gln Lys
            660             665             670
Ser Ile Val Ala Tyr Thr Met Ser Leu Gly Ala Asp Ser Ser Ile Ala
            675             680             685
Tyr Ser Asn Asn Thr Ile Ala Ile Pro Thr Asn Phe Ser Ile Ser Ile
    690             695             700
Thr Thr Glu Val Met Pro Val Ser Met Ala Lys Thr Ser Val Asp Cys
705             710             715             720
Asn Met Tyr Ile Cys Gly Asp Ser Thr Glu Cys Ala Asn Leu Leu Leu
            725             730             735
Gln Tyr Gly Ser Phe Cys Thr Gln Leu Asn Arg Ala Leu Ser Gly Ile
            740             745             750
Ala Ala Glu Gln Asp Arg Asn Thr Arg Glu Val Phe Ala Gln Val Lys
    755             760             765
Gln Met Tyr Lys Thr Pro Thr Leu Lys Tyr Phe Gly Gly Phe Asn Phe
    770             775             780
Ser Gln Ile Leu Pro Asp Pro Leu Lys Pro Thr Lys Arg Ser Phe Ile
785             790             795             800
Glu Asp Leu Leu Phe Asn Lys Val Thr Leu Ala Asp Ala Gly Phe Met
            805             810             815
Lys Gln Tyr Gly Glu Cys Leu Gly Asp Ile Asn Ala Arg Asp Leu Ile
            820             825             830
Cys Ala Gln Lys Phe Asn Gly Leu Thr Val Leu Pro Pro Leu Leu Thr
    835             840             845
Asp Asp Met Ile Ala Ala Tyr Thr Ala Ala Leu Val Ser Gly Thr Ala
    850             855             860
Thr Ala Gly Trp Thr Phe Gly Ala Gly Ala Ala Leu Gln Ile Pro Phe
865             870             875             880
Ala Met Gln Met Ala Tyr Arg Phe Asn Gly Ile Gly Val Thr Gln Asn
            885             890             895
Val Leu Tyr Glu Asn Gln Lys Gln Ile Ala Asn Gln Phe Asn Lys Ala
            900             905             910
Ile Ser Gln Ile Gln Glu Ser Leu Thr Thr Thr Ser Thr Ala Leu Gly
            915             920             925
Lys Leu Gln Asp Val Val Asn Gln Asn Ala Gln Ala Leu Asn Thr Leu
    930             935             940
Val Lys Gln Leu Ser Ser Asn Phe Gly Ala Ile Ser Ser Val Leu Asn
945             950             955             960
Asp Ile Leu Ser Arg Leu Asp Lys Val Glu Ala Glu Val Gln Ile Asp
            965             970             975
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Arg Leu Ile Thr Gly Arg Leu Gln Ser Leu Gln Thr Tyr Val Thr Gln
            980                     985                 990
Gln Leu Ile Arg Ala Ala Glu Ile Arg Ala Ser Ala Asn Leu Ala Ala
            995                 1000                1005
Thr Lys Met Ser Glu Cys Val Leu Gly Gln Ser Lys Arg Val Asp
    1010                1015                1020
Phe Cys Gly Lys Gly Tyr His Leu Met Ser Phe Pro Gln Ala Ala
    1025                1030                1035
Pro His Gly Val Val Phe Leu His Val Thr Tyr Val Pro Ser Gln
    1040                1045                1050
Glu Arg Asn Phe Thr Thr Ala Pro Ala Ile Cys His Glu Gly Lys
    1055                1060                1065
Ala Tyr Phe Pro Arg Glu Gly Val Phe Val Phe Asn Gly Thr Ser
    1070                1075                1080
Trp Phe Ile Thr Gln Arg Asn Phe Phe Ser Pro Gln Ile Ile Thr
    1085                1090                1095
Thr Asp Asn Thr Phe Val Ser Gly Asn Cys Asp Val Val Ile Gly
    1100                1105                1110
Ile Ile Asn Asn Thr Val Tyr Asp Pro Leu Gln Pro Glu Leu Asp
    1115                1120                1125
Ser Phe Lys Glu Glu Leu Asp Lys Tyr Phe Lys Asn His Thr Ser
    1130                1135                1140
Pro Asp Val Asp Leu Gly Asp Ile Ser Gly Ile Asn Ala Ser Val
    1145                1150                1155
Val Asn Ile Gln Lys Glu Ile Asp Arg Leu Asn Glu Val Ala Lys
    1160                1165                1170
Asn Leu Asn Glu Ser Leu Ile Asp Leu Gln Glu Leu Gly Lys Tyr
    1175                1180                1185
Glu Gln Tyr Ile Lys Trp Pro Trp Tyr Val Trp Leu Gly Phe Ile
    1190                1195                1200
Ala Gly Leu Ile Ala Ile Val Met Val Thr Ile Leu Leu Cys Cys
    1205                1210                1215
Met Thr Ser Cys Cys Ser Cys Leu Lys Gly Ala Cys Ser Cys Gly
    1220                1225                1230
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    1235                1240                1245
Gly Val Lys Leu His Tyr Thr
    1250                1255
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<211>   3943
<212>   DNA
<213>   CORONAVIRUS

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gtggtagtga ccttgaccgg tgcaccactt ttgatgatgt tcaagctcct aattacactc    180
aacatacttc atctatgagg ggggtttact atcctgatga aattttttaga tcagacactc    240
tttatttaac tcaggatttta tttcttccat tttattctaa tgttacaggg ttttcatacta    300
ttaatcatac gtttggcaac cctgtcatac cttttaagga tggtatttat tttgctgcca    360
cagagaaatc aaatgttgtc cgtggttggg ttttttggttc taccatgaac aacaagtcac    420
agtcggtgat tattattaac aattctacta atgttgttat acgagcatgt aactttgaat    480
tgtgtgacaa ccctttcttt gctgtttcta aacccatggg tacacagaca catactatga    540
tattcgataa tgcatttaat tgcactttcg agtacatatc tgatgccttt tcgcttgatg    600
tttcagaaaa gtcaggtaat tttaaacact acgagagtt tgtgtttaaa aataaagatg    660
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gttttaacac tttgaaacct atttttaagt tgcctcttgg tattaacatt acaaattttta    780
gagccattct tacagccttt tcacctgctc aagacatttg gggcacgtca gctgcagcct    840
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tcacagatgc tgttgattgt tctcaaaatc cacttgctga actcaaatgc tctgttaaga    960
gctttgagat tgacaaagga atttaccaga cctctaattt cagggttgtt ccctcaggag   1020
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caactggtaa ttataattat aaatataggt atcttagaca tggcaagctt aggccctttg    1440
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<210> 5
<211> 2049
<212> DNA
<213> CORONAVIRUS

<400> 5

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gtggtagtga ccttgaccgg tgcaccactt ttgatgatgt tcaagctcct aattacactc    180
aacatacttc atctatgagg ggggtttact atcctgatga aatttttaga tcagacactc    240
tttatttaac tcaggattta tttcttccat tttattctaa tgttacaggg tttcatacta    300
ttaatcatac gtttggcaac cctgtcatac cttttaagga tggtatttat tttgctgcca    360
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tgtgtgacaa cccttctttt gctgtttcta aacccatggg tacacagaca catactatga      540
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caactggtaa ttataattat aaatataggt atcttagaca tggcaagctt aggccctttg     1440
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cagatcaact cacaccagct tggcgcatat attctactgg aaacaatgta ttccagactc     1980
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<210> 6
<211> 2027
<212> DNA
<213> CORONAVIRUS

<400> 6

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cctattggag ctggcatttg tgctagttac catacagttt ctttattacg tagtactagc      180
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atggttacaa tcttgctttg ttgcatgact agttgttgca gttgcctcaa gggtgcatgc   .1860
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aaattacatt acacataaac gaacttatgg atttgtttat gagatttttt actcttggat   1980
caattactgc acagccagta aaaattgaca atgcttctcc tgcaagt              2027
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<210> 7
<211> 1096
<212> DNA
<213> CORONAVIRUS

<400> 7
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acacataaac gaacttatgg atttgtttat gagatttttt actcttggat caattactgc    180
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<210> 8
<211> 1135
<212> DNA
<213> CORONAVIRUS

<400> 8
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gctggcacac acataactat gactactgta taccatataa cagtgtcaca gatacaattg    660
tcgttactga aggtgacggc atttcaacac caaaactcaa agaagactac caaattggtg    720
gttattctga ggataggcac tcaggtgtta agactatgt cgttgtacat ggctatttca    780
ccgaagttta ctaccagctt gagtctacac aaattactac agacactggt attgaaaatg    840
ctacattctt catctttaac aagcttgtta agacccacc gaatgtgcaa atacacacaa    900
tcgacggctc ttcaggagtt gctaatccag caatggatcc aatttatgat gagccgacga    960
cgactactag cgtgcctttg taagcacaag aaagtgagta cgaacttatg tactcattcg   1020
tttcggaaga aacaggtacg ttaatagtta atagcgtact tcttttcttt gctttcgtgg   1080
tattcttgct agtcacacta gccatcctta ctgcgcttcg attgtgtgcg tactg         1135
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```
<210>  9
<211>  1096
<212>  DNA
<213>  CORONAVIRUS

<220>
<221>  CDS
<222>  (137)..(958)
<223>

<400>  9
tcttgctttg ttgcatgact agttgttgca gttgcctcaa gggtgcatgc tcttgtggtt      60
cttgctgcaa gtttgatgag gatgactctg agccagttct caagggtgtc aaattacatt     120
acacataaac gaactt atg gat ttg ttt atg aga ttt ttt act ctt gga tca     172
               Met Asp Leu Phe Met Arg Phe Phe Thr Leu Gly Ser
                1               5                  10
att act gca cag cca gta aaa att gac aat gct tct cct gca agt act        220
Ile Thr Ala Gln Pro Val Lys Ile Asp Asn Ala Ser Pro Ala Ser Thr
            15                  20                  25
gtt cat gct aca gca acg ata ccg cta caa gcc tca ctc cct ttc gga        268
Val His Ala Thr Ala Thr Ile Pro Leu Gln Ala Ser Leu Pro Phe Gly
        30                  35                  40
tgg ctt gtt att ggc gtt gca ttt ctt gct gtt ttt cag agc gct acc        316
Trp Leu Val Ile Gly Val Ala Phe Leu Ala Val Phe Gln Ser Ala Thr
45                  50                  55                  60
aaa ata att gcg ctc aat aaa aga tgg cag cta gcc ctt tat aag ggc        364
Lys Ile Ile Ala Leu Asn Lys Arg Trp Gln Leu Ala Leu Tyr Lys Gly
                65                  70                  75
ttc cag ttc att tgc aat tta ctg ctg cta ttt gtt acc atc tat tca        412
Phe Gln Phe Ile Cys Asn Leu Leu Leu Leu Phe Val Thr Ile Tyr Ser
            80                  85                  90
cat ctt ttg ctt gtc gct gca ggt atg gag gcg caa ttt ttg tac ctc        460
His Leu Leu Leu Val Ala Ala Gly Met Glu Ala Gln Phe Leu Tyr Leu
        95                  100                 105
tat gcc ttg ata tat ttt cta caa tgc atc aac gca tgt aga att att        508
Tyr Ala Leu Ile Tyr Phe Leu Gln Cys Ile Asn Ala Cys Arg Ile Ile
    110                 115                 120
atg aga tgt tgg ctt tgt tgg aag tgc aaa tcc aag aac cca tta ctt        556
Met Arg Cys Trp Leu Cys Trp Lys Cys Lys Ser Lys Asn Pro Leu Leu
125                 130                 135                 140
tat gat gcc aac tac ttt gtt tgc tgg cac aca cat aac tat gac tac        604
Tyr Asp Ala Asn Tyr Phe Val Cys Trp His Thr His Asn Tyr Asp Tyr
                145                 150                 155
tgt ata cca tat aac agt gtc aca gat aca att gtc gtt act gaa ggt        652
Cys Ile Pro Tyr Asn Ser Val Thr Asp Thr Ile Val Val Thr Glu Gly
                160                 165                 170
gac ggc att tca aca cca aaa ctc aaa gaa gac tac caa att ggt ggt        700
Asp Gly Ile Ser Thr Pro Lys Leu Lys Glu Asp Tyr Gln Ile Gly Gly
                175                 180                 185
tat tct gag gat agg cac tca ggt gtt aaa gac tat gtc gtt gta cat        748
Tyr Ser Glu Asp Arg His Ser Gly Val Lys Asp Tyr Val Val Val His
        190                 195                 200
ggc tat ttc acc gaa gtt tac tac cag ctt gag tct aca caa att act        796
Gly Tyr Phe Thr Glu Val Tyr Tyr Gln Leu Glu Ser Thr Gln Ile Thr
205                 210                 215                 220
aca gac act ggt att gaa aat gct aca ttc ttc atc ttt aac aag ctt        844
Thr Asp Thr Gly Ile Glu Asn Ala Thr Phe Phe Ile Phe Asn Lys Leu
                225                 230                 235
gtt aaa gac cca ccg aat gtg caa ata cac aca atc gac ggc tct tca        892
Val Lys Asp Pro Pro Asn Val Gln Ile His Thr Ile Asp Gly Ser Ser
                240                 245                 250
```

21

```
gga gtt gct aat cca gca atg gat cca att tat gat gag ccg acg acg        940
Gly Val Ala Asn Pro Ala Met Asp Pro Ile Tyr Asp Glu Pro Thr Thr
        255                 260                 265
act act agc gtg cct ttg taagcacaag aaagtgagta cgaacttatg              988
Thr Thr Ser Val Pro Leu
        270
tactcattcg tttcggaaga aacaggtacg ttaatagtta atagcgtact tctttttctt    1048
gctttcgtgg tattcttgct agtcacacta gccatcctta ctgcgctt                 1096
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<210> 10
<211> 274
<212> PRT
<213> CORONAVIRUS

<400> 10

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Met Asp Leu Phe Met Arg Phe Phe Thr Leu Gly Ser Ile Thr Ala Gln
1               5                   10                  15
Pro Val Lys Ile Asp Asn Ala Ser Pro Ala Ser Thr Val His Ala Thr
            20                  25                  30
Ala Thr Ile Pro Leu Gln Ala Ser Leu Pro Phe Gly Trp Leu Val Ile
            35                  40                  45
Gly Val Ala Phe Leu Ala Val Phe Gln Ser Ala Thr Lys Ile Ile Ala
        50                  55                  60
Leu Asn Lys Arg Trp Gln Leu Ala Leu Tyr Lys Gly Phe Gln Phe Ile
65                  70                  75                  80
Cys Asn Leu Leu Leu Leu Phe Val Thr Ile Tyr Ser His Leu Leu Leu
                85                  90                  95
Val Ala Ala Gly Met Glu Ala Gln Phe Leu Tyr Leu Tyr Ala Leu Ile
                100                 105                 110
Tyr Phe Leu Gln Cys Ile Asn Ala Cys Arg Ile Ile Met Arg Cys Trp
        115                 120                 125
Leu Cys Trp Lys Cys Lys Ser Lys Asn Pro Leu Leu Tyr Asp Ala Asn
        130                 135                 140
Tyr Phe Val Cys Trp His Thr His Asn Tyr Asp Tyr Cys Ile Pro Tyr
145                 150                 155                 160
Asn Ser Val Thr Asp Thr Ile Val Val Thr Glu Gly Asp Gly Ile Ser
                165                 170                 175
Thr Pro Lys Leu Lys Glu Asp Tyr Gln Ile Gly Gly Tyr Ser Glu Asp
            180                 185                 190
Arg His Ser Gly Val Lys Asp Tyr Val Val Val His Gly Tyr Phe Thr
        195                 200                 205
Glu Val Tyr Tyr Gln Leu Glu Ser Thr Gln Ile Thr Thr Asp Thr Gly
    210                 215                 220
Ile Glu Asn Ala Thr Phe Phe Ile Phe Asn Lys Leu Val Lys Asp Pro
225                 230                 235                 240
Pro Asn Val Gln Ile His Thr Ile Asp Gly Ser Ser Gly Val Ala Asn
            245                 250                 255
Pro Ala Met Asp Pro Ile Tyr Asp Glu Pro Thr Thr Thr Ser Val
            260                 265                 270
Pro Leu
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<210> 11
<211> 1096
<212> DNA
<213> CORONAVIRUS

<220>
<221> CDS
<222> (558)..(1019)
<223>
<400> 11

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tcttgctttg ttgcatgact agttgttgca gttgcctcaa gggtgcatgc tcttgtggtt      60
cttgctgcaa gtttgatgag gatgactctg agccagttct caagggtgtc aaattacatt     120
acacataaac gaacttatgg atttgtttat gagatttttt actcttggat caattactgc     180
acagccagta aaaattgaca atgcttctcc tgcaagtact gttcatgcta cagcaacgat     240
accgctacaa gcctcactcc ctttcggatg gcttgttatt ggcgttgcat ttcttgctgt     300
ttttcagagc gctaccaaaa taattgcgct caataaaaga tggcagctag ccctttataa     360
gggcttccag ttcatttgca atttactgct gctatttgtt accatctatt cacatctttt     420
gcttgtcgct gcaggtatgg aggcgcaatt tttgtacctc tatgccttga tatattttct     480
acaatgcatc aacgcatgta gaattattat gagatgttgg ctttgttgga agtgcaaatc     540
caagaaccca ttacttt atg atg cca act act ttg ttt gct ggc aca cac       590
                    Met Met Pro Thr Thr Leu Phe Ala Gly Thr His
                     1           5                   10

ata act atg act act gta tac cat ata aca gtg tca cag ata caa ttg      638
Ile Thr Met Thr Thr Val Tyr His Ile Thr Val Ser Gln Ile Gln Leu
            15              20              25

tcg tta ctg aag gtg acg gca ttt caa cac caa aac tca aag aag act      686
Ser Leu Leu Lys Val Thr Ala Phe Gln His Gln Asn Ser Lys Lys Thr
        30              35              40

acc aaa ttg gtg gtt att ctg agg ata ggc act cag gtg tta aag act      734
Thr Lys Leu Val Val Ile Leu Arg Ile Gly Thr Gln Val Leu Lys Thr
    45              50              55

atg tcg ttg tac atg gct att tca ccg aag ttt act acc agc ttg agt      782
Met Ser Leu Tyr Met Ala Ile Ser Pro Lys Phe Thr Thr Ser Leu Ser
60              65              70                  75

cta cac aaa tta cta cag aca ctg gta ttg aaa atg cta cat tct tca      830
Leu His Lys Leu Leu Gln Thr Leu Val Leu Lys Met Leu His Ser Ser
            80              85                  90

tct tta aca agc ttg tta aag acc cac cga atg tgc aaa tac aca caa      878
Ser Leu Thr Ser Leu Leu Lys Thr His Arg Met Cys Lys Tyr Thr Gln
        95              100             105

tcg acg gct ctt cag gag ttg cta atc cag caa tgg atc caa ttt atg      926
Ser Thr Ala Leu Gln Glu Leu Leu Ile Gln Gln Trp Ile Gln Phe Met
        110             115             120

atg agc cga cga cga cta cta gcg tgc ctt tgt aag cac aag aaa gtg      974
Met Ser Arg Arg Arg Leu Leu Ala Cys Leu Cys Lys His Lys Lys Val
    125             130             135

agt acg aac tta tgt act cat tcg ttt cgg aag aaa cag gta cgt        1019
Ser Thr Asn Leu Cys Thr His Ser Phe Arg Lys Lys Gln Val Arg
140             145             150

taatagttaa tagcgtactt cttttcttg ctttcgtggt attcttgcta gtcacactag    1079
ccatccttac tgcgctt                                                   1096
```

<210> 12
<211> 154
<212> PRT
<213> CORONAVIRUS

<400> 12
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Met Met Pro Thr Thr Leu Phe Ala Gly Thr His Ile Thr Met Thr Thr
1               5                   10                  15
Val Tyr His Ile Thr Val Ser Gln Ile Gln Leu Ser Leu Leu Lys Val
            20                  25                  30
Thr Ala Phe Gln His Gln Asn Ser Lys Lys Thr Thr Lys Leu Val Val
            35                  40                  45
Ile Leu Arg Ile Gly Thr Gln Val Leu Lys Thr Met Ser Leu Tyr Met
    50                  55                  60
Ala Ile Ser Pro Lys Phe Thr Thr Ser Leu Ser Leu His Lys Leu Leu
65                  70                  75                  80
Gln Thr Leu Val Leu Lys Met Leu His Ser Ser Ser Leu Thr Ser Leu
            85                  90                  95
Leu Lys Thr His Arg Met Cys Lys Tyr Thr Gln Ser Thr Ala Leu Gln
            100                 105                 110
```

```
Glu Leu Leu Ile Gln Gln Trp Ile Gln Phe Met Met Ser Arg Arg Arg
        115             120             125
Leu Leu Ala Cys Leu Cys Lys His Lys Lys Val Ser Thr Asn Leu Cys
        130             135             140
Thr His Ser Phe Arg Lys Lys Gln Val Arg
145             150
```

<210> 13
<211> 332
<212> DNA
<213> CORONAVIRUS

<220>
<221> CDS
<222> (36)..(263)
<223>

<400> 13

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tgcctttgta agcacaagaa agtgagtacg aactt atg tac tca ttc gtt tcg      53
                                        Met Tyr Ser Phe Val Ser
                                         1           5
gaa gaa aca ggt acg tta ata gtt aat agc gta ctt ctt ttt ctt gct    101
Glu Glu Thr Gly Thr Leu Ile Val Asn Ser Val Leu Leu Phe Leu Ala
            10              15              20
ttc gtg gta ttc ttg cta gtc aca cta gcc atc ctt act gcg ctt cga    149
Phe Val Val Phe Leu Leu Val Thr Leu Ala Ile Leu Thr Ala Leu Arg
            25              30              35
ttg tgt gcg tac tgc tgc aat att gtt aac gtg agt tta gta aaa cca    197
Leu Cys Ala Tyr Cys Cys Asn Ile Val Asn Val Ser Leu Val Lys Pro
        40              45              50
acg gtt tac gtc tac tcg cgt gtt aaa aat ctg aac tct tct gaa gga    245
Thr Val Tyr Val Tyr Ser Arg Val Lys Asn Leu Asn Ser Ser Glu Gly
55              60              65                      70
gtt cct gat ctt ctg gtc taaacgaact aactattatt attattctgt          293
Val Pro Asp Leu Leu Val
                75
ttggaacttt aacattgctt atcatggcag acaacggta                          332
```

<210> 14
<211> 76
<212> PRT
<213> CORONAVIRUS

<400> 14

```
Met Tyr Ser Phe Val Ser Glu Glu Thr Gly Thr Leu Ile Val Asn Ser
1               5               10              15
Val Leu Leu Phe Leu Ala Phe Val Val Phe Leu Leu Val Thr Leu Ala
            20              25              30
Ile Leu Thr Ala Leu Arg Leu Cys Ala Tyr Cys Cys Asn Ile Val Asn
        35              40              45
Val Ser Leu Val Lys Pro Thr Val Tyr Val Tyr Ser Arg Val Lys Asn
    50              55              60
Leu Asn Ser Ser Glu Gly Val Pro Asp Leu Leu Val
65              70              75
```

<210> 15
<211> 332
<212> DNA
<213> CORONAVIRUS

<400> 15

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tgcctttgta agcacaagaa agtgagtacg aacttatgta ctcattcgtt tcggaagaaa    60
```

```
caggtacgtt aatagttaat agcgtacttc tttttcttgc tttcgtggta ttcttgctag    120
tcacactagc catccttact gcgcttcgat tgtgtgcgta ctgctgcaat attgttaacg    180
tgagtttagt aaaaccaacg gtttacgtct actcgcgtgt taaaaatctg aactcttctg    240
aaggagttcc tgatcttctg gtctaaacga actaactatt attattattc tgtttggaac    300
tttaacattg cttatcatgg cagacaacgg ta                                  332
```

<210> 16
<211> 708
<212> DNA
<213> CORONAVIRUS

<220>
<221> CDS
<222> (41)..(703)
<223>

<400> 16

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tattattatt attctgtttg gaactttaac attgcttatc atg gca gac aac ggt      55
                                                 Met Ala Asp Asn Gly
                                                 1               5

act att acc gtt gag gag ctt aaa caa ctc ctg gaa caa tgg aac cta     103
Thr Ile Thr Val Glu Glu Leu Lys Gln Leu Leu Glu Gln Trp Asn Leu
                10                  15                  20

gta ata ggt ttc cta ttc cta gcc tgg att atg tta cta caa ttt gcc     151
Val Ile Gly Phe Leu Phe Leu Ala Trp Ile Met Leu Leu Gln Phe Ala
            25                  30                  35

tat tct aat cgg aac agg ttt ttg tac ata ata aag ctt gtt ttc ctc     199
Tyr Ser Asn Arg Asn Arg Phe Leu Tyr Ile Ile Lys Leu Val Phe Leu
            40                  45                  50

tgg ctc ttg tgg cca gta aca ctt gct tgt ttt gtg ctt gct gct gtc     247
Trp Leu Leu Trp Pro Val Thr Leu Ala Cys Phe Val Leu Ala Ala Val
    55                  60                  65

tac aga att aat tgg gtg act ggc ggg att gcg att gca atg gct tgt     295
Tyr Arg Ile Asn Trp Val Thr Gly Gly Ile Ala Ile Ala Met Ala Cys
70                  75                  80                  85

att gta ggc ttg atg tgg ctt agc tac ttc gtt gct tcc ttc agg ctg     343
Ile Val Gly Leu Met Trp Leu Ser Tyr Phe Val Ala Ser Phe Arg Leu
                90                  95                  100

ttt gct cgt acc cgc tca atg tgg tca ttc aac cca gaa aca aac att     391
Phe Ala Arg Thr Arg Ser Met Trp Ser Phe Asn Pro Glu Thr Asn Ile
            105                 110                 115

ctt ctc aat gtg cct ctc cgg ggg aca att gtg acc aga ccg ctc atg     439
Leu Leu Asn Val Pro Leu Arg Gly Thr Ile Val Thr Arg Pro Leu Met
            120                 125                 130

gaa agt gaa ctt gtc att ggt gct gtg atc att cgt ggt cac ttg cga     487
Glu Ser Glu Leu Val Ile Gly Ala Val Ile Ile Arg Gly His Leu Arg
        135                 140                 145

atg gcc gga cac tcc cta ggg cgc tgt gac att aag gac ctg cca aaa     535
Met Ala Gly His Ser Leu Gly Arg Cys Asp Ile Lys Asp Leu Pro Lys
150                 155                 160                 165

gag atc act gtg gct aca tca cga acg ctt tct tat tac aaa tta gga     583
Glu Ile Thr Val Ala Thr Ser Arg Thr Leu Ser Tyr Tyr Lys Leu Gly
            170                 175                 180

gcg tcg cag cgt gta ggc act gat tca ggt ttt gct gca tac aac cgc     631
Ala Ser Gln Arg Val Gly Thr Asp Ser Gly Phe Ala Ala Tyr Asn Arg
            185                 190                 195

tac cgt att gga aac tat aaa tta aat aca gac cac gcc ggt agc aac     679
Tyr Arg Ile Gly Asn Tyr Lys Leu Asn Thr Asp His Ala Gly Ser Asn
            200                 205                 210

gac aat att gct ttg cta gta cag taagt                               708
Asp Asn Ile Ala Leu Leu Val Gln
    215                 220
```

```
<210>  17
<211>  221
<212>  PRT
<213>  CORONAVIRUS

<400>  17
Met Ala Asp Asn Gly Thr Ile Thr Val Glu Glu Leu Lys Gln Leu Leu
1               5                   10                  15
Glu Gln Trp Asn Leu Val Ile Gly Phe Leu Phe Leu Ala Trp Ile Met
            20                  25                  30
Leu Leu Gln Phe Ala Tyr Ser Asn Arg Asn Arg Phe Leu Tyr Ile Ile
        35                  40                  45
Lys Leu Val Phe Leu Trp Leu Leu Trp Pro Val Thr Leu Ala Cys Phe
    50                  55                  60
Val Leu Ala Ala Val Tyr Arg Ile Asn Trp Val Thr Gly Gly Ile Ala
65                  70                  75                  80
Ile Ala Met Ala Cys Ile Val Gly Leu Met Trp Leu Ser Tyr Phe Val
                85                  90                  95
Ala Ser Phe Arg Leu Phe Ala Arg Thr Arg Ser Met Trp Ser Phe Asn
            100                 105                 110
Pro Glu Thr Asn Ile Leu Leu Asn Val Pro Leu Arg Gly Thr Ile Val
            115                 120                 125
Thr Arg Pro Leu Met Glu Ser Glu Leu Val Ile Gly Ala Val Ile Ile
    130                 135                 140
Arg Gly His Leu Arg Met Ala Gly His Ser Leu Gly Arg Cys Asp Ile
145                 150                 155                 160
Lys Asp Leu Pro Lys Glu Ile Thr Val Ala Thr Ser Arg Thr Leu Ser
                165                 170                 175
Tyr Tyr Lys Leu Gly Ala Ser Gln Arg Val Gly Thr Asp Ser Gly Phe
            180                 185                 190
Ala Ala Tyr Asn Arg Tyr Arg Ile Gly Asn Tyr Lys Leu Asn Thr Asp
            195                 200                 205
His Ala Gly Ser Asn Asp Asn Ile Ala Leu Leu Val Gln
    210                 215                 220

<210>  18
<211>  769
<212>  DNA
<213>  CORONAVIRUS

<400>  18
cctgatcttc tggtctaaac gaactaacta ttattattat tctgtttgga actttaacat      60
tgcttatcat ggcagacaac ggtactatta ccgttgagga gcttaaacaa ctcctggaac     120
aatggaacct agtaataggt ttcctattcc tagcctggat tatgttacta caatttgcct     180
attctaatcg gaacaggttt ttgtacataa taaagcttgt tttcctctgg ctcttgtggc     240
cagtaacact tgcttgtttt gtgcttgctg ctgtctacag aattaattgg gtgactggcg     300
ggattgcgat tgcaatggct tgtattgtag gcttgatgtg gcttagctac ttcgttgctt     360
ccttcaggct gtttgctcgt acccgctcaa tgtggtcatt caacccagaa acaaacattc     420
ttctcaatgt gcctctccgg gggacaattg tgaccagacc gctcatggaa agtgaacttg     480
tcattggtgc tgtgatcatt cgtggtcact tgcgaatggc cggacactcc ctagggcgct     540
gtgacattaa ggacctgcca aaagagatca ctgtggctac atcacgaacg ctttcttatt     600
acaaattagg agcgtcgcag cgtgtaggca ctgattcagg ttttgctgca tacaaccgct     660
accgtattgg aaactataaa ttaaatacag accacgccgg tagcaacgac aatattgctt     720
tgctagtaca gtaagtgaca acagatgttt catcttgttg acttccagg                 769

<210>  19
<211>  1231
<212>  DNA
<213>  CORONAVIRUS

<400>  19
taccgtattg gaaactataa attaaataca gaccacgccg gtagcaacga caatattgct      60
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ttgctagtac agtaagtgac aacagatgtt tcatcttgtt gacttccagg ttacaatagc    120
agagatattg attatcatta tgaggacttt caggattgct atttggaatc ttgacgttat    180
aataagttca atagtgagac aattatttaa gcctctaact aagaagaatt attcggagtt    240
agatgatgaa gaacctatgg agttagatta tccataaaac gaacatgaaa attattctct    300
tcctgacatt gattgtattt acatcttgcg agctatatca ctatcaggag tgtgttagag    360
gtacgactgt actactaaaa gaaccttgcc catcaggaac atacgagggc aattcaccat    420
ttcaccctct tgctgacaat aaatttgcac taacttgcac tagcacacac tttgcttttg    480
cttgtgctga cggtactcga catacctatc agctgcgtgc aagatcagtt tcaccaaaac    540
ttttcatcag acaagaggag gttcaacaag agctctactc gccacttttt ctcattgttg    600
ctgctctagt atttttaata ctttgcttca ccattaagag aaagacagaa tgaatgagct    660
cactttaatt gacttctatt tgtgcttttt agcctttctg ctattccttg ttttaataat    720
gcttattata ttttggtttt cactcgaaat ccaggatcta gaagaacctt gtaccaaagt    780
ctaaacgaac atgaaacttc tcattgtttt gacttgtatt tctctatgca gttgcatatg    840
cactgtagta cagcgctgtg catctaataa acctcatgtg cttgaagatc cttgtaaggt    900
acaacactag gggtaatact tatagcactg cttggctttg tgctctagga aaggttttac    960
cttttcatag atggcacact atggttcaaa catgcacacc taatgttact atcaactgtc   1020
aagatccagc tggtggtgcg cttatagcta ggtgttggta ccttcatgaa ggtcaccaaa   1080
ctgctgcatt tagagacgta cttgttgttt aaataaacg aacaaattaa aatgtctgat   1140
aatggacccc aatcaaacca acgtagtgcc ccccgcatta catttggtgg acccacagat   1200
tcaactgaca ataaccagaa tggaggacgc a                                  1231
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<210> 20
<211> 1242
<212> DNA
<213> CORONAVIRUS

<400> 20
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gcatacaacc gctaccgtat tggaaactat aaattaaata cagaccacgc cggtagcaac     60
gacaatattg ctttgctagt acagtaagtg acaacagatg tttcatcttg ttgacttcca    120
ggttacaata gcagagatat tgattatcat tatgaggact ttcaggattg ctatttggaa    180
tcttgacgtt ataataagtt caatagtgag acagttattt aagcctctaa ctaagaagaa    240
ttattcggag ttagatgatg aagaacctat ggagttagat tatccataaa acgaacatga    300
aaattattct cttcctgaca ttgattgtat ttacatcttg cgagctatat cactatcagg    360
agtgtgttag aggtacgact gtactactaa aagaaccttg cccatcagga acatacgagg    420
gcaattcacc atttcaccct cttgctgaca ataaatttgc actaacttgc actagcacac    480
actttgcttt tgcttgtgct gacggtactc gacatacctg tcagctgcgt gcaagatcag    540
tttcaccaaa actttcatc agacaagagg aggttcaaca agagctctac tcgccacttt    600
ttctcattgt tgctgctcta gtattttaa tactttgctt caccattaag agaaagacag    660
aatgaatgag ctcactttaa ttgacttcta tttgtgcttt ttagcctttc tgctattcct    720
tgtttaata atgcttatta tattttggtt ttcactcgaa atccaggatc tagaagaacc    780
ttgtaccaaa gtctaaacga acatgaaact tctcattgtt ttgacttgta tttctctatg    840
cagttgcata tgcactgtag tacagcgctg tgcatctaat aaacctcatg tgcttgaaga    900
tccttgtaag gtacaacact aggggtaata cttatagcac tgcttggctt tgtgctctag    960
gaaaggtttt accttttcat agatggcaca ctatggttca aacatgcaca cctaatgtta   1020
ctatcaactg tcaagatcca gctggtggtg cgcttatagc taggtgttgg taccttcatg   1080
aaggtcacca aactgctgca tttagagacg tacttgttgt tttaaataaa cgaacgaatt   1140
aaaatgtctg ataatggacc ccaatcaaac caacgtagtg ccccccgcat tacatttggt   1200
ggacccacag attcaactga caataaccag aatggaggac gc                      1242
```

<210>   21
<211>   1231
<212>   DNA
<213>   CORONAVIRUS

<220>
<221>   CDS
<222>   (86)..(274)
<223>
<400>   21
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taccgtattg gaaactataa attaaataca gaccacgccg gtagcaacga caatattgct     60
```

```
ttgctagtac agtaagtgac aacag atg ttt cat ctt gtt gac ttc cag gtt          112
                            Met Phe His Leu Val Asp Phe Gln Val
                            1               5

aca ata gca gag ata ttg att atc att atg agg act ttc agg att gct          160
Thr Ile Ala Glu Ile Leu Ile Ile Ile Met Arg Thr Phe Arg Ile Ala
10              15              20              25

att tgg aat ctt gac gtt ata ata agt tca ata gtg aga caa tta ttt          208
Ile Trp Asn Leu Asp Val Ile Ile Ser Ser Ile Val Arg Gln Leu Phe
                30              35              40

aag cct cta act aag aag aat tat tcg gag tta gat gat gaa gaa cct          256
Lys Pro Leu Thr Lys Lys Asn Tyr Ser Glu Leu Asp Asp Glu Glu Pro
                45              50              55

atg gag tta gat tat cca taaaacgaac atgaaaatta ttctcttcct               304
Met Glu Leu Asp Tyr Pro
            60

gacattgatt gtatttacat cttgcgagct atatcactat caggagtgtg ttagaggtac        364
gactgtacta ctaaaagaac cttgcccatc aggaacatac gagggcaatt caccatttca        424
ccctcttgct gacaataaat ttgcactaac ttgcactagc acacactttg cttttgcttg        484
tgctgacggt actcgacata cctatcagct gcgtgcaaga tcagtttcac caaaactttt        544
catcagacaa gaggaggttc aacaagagct ctactcgcca ctttttctca ttgttgctgc        604
tctagtattt ttaatacttt gcttcaccat taagagaaag acagaatgaa tgagctcact        664
ttaattgact tctatttgtg ctttttagcc tttctgctat tccttgtttt aataatgctt        724
attatatttt ggttttcact cgaaatccag gatctagaag aaccttgtac caaagtctaa        784
acgaacatga aacttctcat tgttttgact tgtatttctc tatgcagttg catatgcact        844
gtagtacagc gctgtgcatc taataaacct catgtgcttg aagatccttg taaggtacaa        904
cactaggggt aatacttata gcactgcttg ctttgtgct ctaggaaagg ttttaccttt        964
tcatagatgg cacactatgg ttcaaacatg cacacctaat gttactatca actgtcaaga       1024
tccagctggt ggtgcgctta tagctaggtg ttggtacctt catgaaggtc accaaactgc       1084
tgcatttaga gacgtacttg ttgttttaaa taaacgaaca aattaaaatg tctgataatg       1144
gaccccaatc aaaccaacgt agtgcccccc gcattacatt tggtggaccc acagattcaa       1204
ctgacaataa ccagaatgga ggacgca                                          1231
```

```
<210>  22
<211>  63
<212>  PRT
<213>  CORONAVIRUS

<400>  22
Met Phe His Leu Val Asp Phe Gln Val Thr Ile Ala Glu Ile Leu Ile
1               5                   10              15
Ile Ile Met Arg Thr Phe Arg Ile Ala Ile Trp Asn Leu Asp Val Ile
            20              25              30
Ile Ser Ser Ile Val Arg Gln Leu Phe Lys Pro Leu Thr Lys Lys Asn
            35              40              45
Tyr Ser Glu Leu Asp Asp Glu Glu Pro Met Glu Leu Asp Tyr Pro
    50              55              60
```

```
<210>  23
<211>  1231
<212>  DNA
<213>  CORONAVIRUS

<220>
<221>  CDS
<222>  (285)..(650)
<223>

<400>  23
taccgtattg gaaactataa attaaataca gaccacgccg gtagcaacga caatattgct          60
ttgctagtac agtaagtgac aacagatgtt tcatcttgtt gacttccagg ttacaatagc        120
agagatattg attatcatta tgaggacttt caggattgct atttggaatc ttgacgttat        180
aataagttca atagtgagac aattatttaa gcctctaact aagaagaatt attcggagtt        240
```

```
agatgatgaa gaacctatgg agttagatta tccataaaac gaac atg aaa att att        296
                                                    Met Lys Ile Ile
                                                      1
ctc ttc ctg aca ttg att gta ttt aca tct tgc gag cta tat cac tat        344
Leu Phe Leu Thr Leu Ile Val Phe Thr Ser Cys Glu Leu Tyr His Tyr
  5                   10                  15                  20
cag gag tgt gtt aga ggt acg act gta cta cta aaa gaa cct tgc cca        392
Gln Glu Cys Val Arg Gly Thr Thr Val Leu Leu Lys Glu Pro Cys Pro
                 25                  30                  35
tca gga aca tac gag ggc aat tca cca ttt cac cct ctt gct gac aat        440
Ser Gly Thr Tyr Glu Gly Asn Ser Pro Phe His Pro Leu Ala Asp Asn
                 40                  45                  50
aaa ttt gca cta act tgc act agc aca cac ttt gct ttt gct tgt gct        488
Lys Phe Ala Leu Thr Cys Thr Ser Thr His Phe Ala Phe Ala Cys Ala
                 55                  60                  65
gac ggt act cga cat acc tat cag ctg cgt gca aga tca gtt tca cca        536
Asp Gly Thr Arg His Thr Tyr Gln Leu Arg Ala Arg Ser Val Ser Pro
     70                  75                  80
aaa ctt ttc atc aga caa gag gag gtt caa caa gag ctc tac tcg cca        584
Lys Leu Phe Ile Arg Gln Glu Glu Val Gln Gln Glu Leu Tyr Ser Pro
 85                  90                  95                 100
ctt ttt ctc att gtt gct gct cta gta ttt tta ata ctt tgc ttc acc        632
Leu Phe Leu Ile Val Ala Ala Leu Val Phe Leu Ile Leu Cys Phe Thr
                105                 110                 115
att aag aga aag aca gaa tgaatgagct cactttaatt gacttctatt             680
Ile Lys Arg Lys Thr Glu
                120
tgtgcttttt agcctttctg ctattccttg ttttaataat gcttattata ttttggtttt      740
cactcgaaat ccaggatcta gaagaacctt gtaccaaagt ctaaacgaac atgaaacttc      800
tcattgtttt gacttgtatt tctctatgca gttgcatatg cactgtagta cagcgctgtg      860
catctaataa acctcatgtg cttgaagatc cttgtaaggt acaacactag gggtaatact      920
tatagcactg cttggctttg tgctctagga aaggttttac cttttcatag atggcacact      980
atggttcaaa catgcacacc taatgttact atcaactgtc aagatccagc tggtggtgcg     1040
cttatagcta ggtgttggta ccttcatgaa ggtcaccaaa ctgctgcatt tagagacgta     1100
cttgttgttt taaataaacg aacaaattaa aatgtctgat aatggacccc aatcaaacca     1160
acgtagtgcc ccccgcatta catttggtgg acccacagat tcaactgaca ataaccagaa     1220
tggaggacgc a                                                          1231
```

<210> 24
<211> 122
<212> PRT
<213> CORONAVIRUS

<400> 24

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Met Lys Ile Ile Leu Phe Leu Thr Leu Ile Val Phe Thr Ser Cys Glu
  1               5                  10                  15
Leu Tyr His Tyr Gln Glu Cys Val Arg Gly Thr Thr Val Leu Leu Lys
                 20                  25                  30
Glu Pro Cys Pro Ser Gly Thr Tyr Glu Gly Asn Ser Pro Phe His Pro
                 35                  40                  45
Leu Ala Asp Asn Lys Phe Ala Leu Thr Cys Thr Ser Thr His Phe Ala
     50                  55                  60
Phe Ala Cys Ala Asp Gly Thr Arg His Thr Tyr Gln Leu Arg Ala Arg
 65                  70                  75                  80
Ser Val Ser Pro Lys Leu Phe Ile Arg Gln Glu Glu Val Gln Gln Glu
                 85                  90                  95
Leu Tyr Ser Pro Leu Phe Leu Ile Val Ala Ala Leu Val Phe Leu Ile
                100                 105                 110
Leu Cys Phe Thr Ile Lys Arg Lys Thr Glu
                115                 120
```

<210> 25
<211> 1231

<212> DNA
<213> CORONAVIRUS

<220>
<221> CDS
<222> (650)..(781)
<223>

<400> 25
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taccgtattg gaaactataa attaaataca gaccacgccg gtagcaacga caatattgct    60
ttgctagtac agtaagtgac aacagatgtt tcatcttgtt gacttccagg ttacaatagc   120
agagatattg attatcatta tgaggacttt caggattgct atttggaatc ttgacgttat   180
aataagttca atagtgagac aattatttaa gcctctaact aagaagaatt attcggagtt   240
agatgatgaa gaacctatgg agttagatta tccataaaac gaacatgaaa attattctct   300
tcctgacatt gattgtattt acatcttgcg agctatatca ctatcaggag tgtgttagag   360
gtacgactgt actactaaaa gaaccttgcc catcaggaac atacgagggc aattcaccat   420
ttcaccctct tgctgacaat aaatttgcac taacttgcac tagcacacac tttgcttttg   480
cttgtgctga cggtactcga cataccatc agctgcgtgc aagatcagtt tcaccaaaac    540
ttttcatcag acaagaggag gttcaacaag agctctactc gccacttttt ctcattgttg    600
ctgctctagt attttaata ctttgcttca ccattaagag aaagacaga atg aat gag   658
                                                        Met Asn Glu
                                                          1
ctc act tta att gac ttc tat ttg tgc ttt tta gcc ttt ctg cta ttc    706
Leu Thr Leu Ile Asp Phe Tyr Leu Cys Phe Leu Ala Phe Leu Leu Phe
      5               10                  15
ctt gtt tta ata atg ctt att ata ttt tgg ttt tca ctc gaa atc cag    754
Leu Val Leu Ile Met Leu Ile Ile Phe Trp Phe Ser Leu Glu Ile Gln
20               25                  30                  35
gat cta gaa gaa cct tgt acc aaa gtc taaacgaaca tgaaacttct            801
Asp Leu Glu Glu Pro Cys Thr Lys Val
                40
cattgttttg acttgtattt ctctatgcag ttgcatatgc actgtagtac agcgctgtgc   861
atctaataaa cctcatgtgc ttgaagatcc ttgtaaggta caacactagg ggtaatactt   921
atagcactgc ttggctttgt gctctaggaa aggttttacc ttttcataga tggcacacta   981
tggttcaaac atgcacacct aatgttacta tcaactgtca agatccagct ggtggtgcgc  1041
ttatagctag gtgttggtac cttcatgaag gtcaccaaac tgctgcattt agagacgtac  1101
ttgttgtttt aaataaacga acaaattaaa atgtctgata atggacccca atcaaaccaa  1161
cgtagtgccc cccgcattac atttggtgga cccacagatt caactgacaa taaccagaat  1221
ggaggacgca                                                        1231
```

<210> 26
<211> 44
<212> PRT
<213> CORONAVIRUS

<400> 26
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Met Asn Glu Leu Thr Leu Ile Asp Phe Tyr Leu Cys Phe Leu Ala Phe
1               5                   10                  15
Leu Leu Phe Leu Val Leu Ile Met Leu Ile Ile Phe Trp Phe Ser Leu
              20                  25                  30
Glu Ile Gln Asp Leu Glu Glu Pro Cys Thr Lys Val
              35                  40
```

<210> 27
<211> 1231
<212> DNA
<213> CORONAVIRUS

<220>
<221> CDS
<222> (791)..(907)
<223>

<400> 27
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taccgtattg gaaactataa attaaataca gaccacgccg gtagcaacga caatattgct    60
ttgctagtac agtaagtgac aacagatgtt tcatcttgtt gacttccagg ttacaatagc   120
agagatattg attatcatta tgaggacttt caggattgct atttggaatc ttgacgttat   180
aataagttca atagtgagac aattatttaa gcctctaact aagaagaatt attcggagtt   240
agatgatgaa gaacctatgg agttagatta tccataaaac gaacatgaaa attattctct   300
tcctgacatt gattgtattt acatcttgcg agctatatca ctatcaggag tgtgttagag   360
gtacgactgt actactaaaa gaaccttgcc catcaggaac atacgagggc aattcaccat   420
ttcaccctct tgctgacaat aaatttgcac taacttgcac tagcacacac tttgcttttg   480
cttgtgctga cggtactcga catacctatc agctgcgtgc aagatcagtt tcaccaaaac   540
ttttcatcag acaagaggag gttcaacaag agctctactc gccacttttt ctcattgttg   600
ctgctctagt attttttaata ctttgcttca ccattaagag aaagacagaa tgaatgagct   660
cactttaatt gacttctatt tgtgcttttt agcctttctg ctattccttg ttttaataat   720
gcttattata ttttggtttt cactcgaaat ccaggatcta gaagaacctt gtaccaaagt   780
ctaaacgaac atg aaa ctt ctc att gtt ttg act tgt att tct cta tgc   829
            Met Lys Leu Leu Ile Val Leu Thr Cys Ile Ser Leu Cys
            1               5                   10
agt tgc ata tgc act gta gta cag cgc tgt gca tct aat aaa cct cat   877
Ser Cys Ile Cys Thr Val Val Gln Arg Cys Ala Ser Asn Lys Pro His
    15                  20                  25
gtg ctt gaa gat cct tgt aag gta caa cac tagggtaat acttatagca   927
Val Leu Glu Asp Pro Cys Lys Val Gln His
30                  35
ctgcttggct ttgtgctcta ggaaaggttt tacctttca tagatggcac actatggttc   987
aaacatgcac acctaatgtt actatcaact gtcaagatcc agctggtggt gcgcttatag  1047
ctaggtgttg gtaccttcat gaaggtcacc aaactgctgc atttagagac gtacttgttg  1107
ttttaaataa acgaacaaat taaaatgtct gataatggac cccaatcaaa ccaacgtagt  1167
gcccccccgca ttacatttgg tggacccaca gattcaactg acaataacca gaatggagga  1227
cgca                                                               1231
```

<210> 28
<211> 39
<212> PRT
<213> CORONAVIRUS

<400> 28
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Met Lys Leu Leu Ile Val Leu Thr Cys Ile Ser Leu Cys Ser Cys Ile
1               5                   10                  15
Cys Thr Val Val Gln Arg Cys Ala Ser Asn Lys Pro His Val Leu Glu
            20                  25                  30
Asp Pro Cys Lys Val Gln His
            35
```

<210> 29
<211> 1231
<212> DNA
<213> CORONAVIRUS

<220>
<221> CDS
<222> (876)..(1127)
<223>

<400> 29
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taccgtattg gaaactataa attaaataca gaccacgccg gtagcaacga caatattgct    60
ttgctagtac agtaagtgac aacagatgtt tcatcttgtt gacttccagg ttacaatagc   120
agagatattg attatcatta tgaggacttt caggattgct atttggaatc ttgacgttat   180
aataagttca atagtgagac aattatttaa gcctctaact aagaagaatt attcggagtt   240
agatgatgaa gaacctatgg agttagatta tccataaaac gaacatgaaa attattctct   300
tcctgacatt gattgtattt acatcttgcg agctatatca ctatcaggag tgtgttagag   360
gtacgactgt actactaaaa gaaccttgcc catcaggaac atacgagggc aattcaccat   420
ttcaccctct tgctgacaat aaatttgcac taacttgcac tagcacacac tttgcttttg   480
```

cttgtgctga cggtactcga catacctatc agctgcgtgc aagatcagtt tcaccaaaac 540
ttttcatcag acaagaggag gttcaacaag agctctactc gccacttttt ctcattgttg 600
ctgctctagt atttttaata ctttgcttca ccattaagag aaagacagaa tgaatgagct 660
cactttaatt gacttctatt tgtgcttttt agcctttctg ctattccttg ttttaataat 720
gcttattata ttttggtttt cactcgaaat ccaggatcta gaagaacctt gtaccaaagt 780
ctaaacgaac atgaaacttc tcattgtttt gacttgtatt tctctatgca gttgcatatg 840
cactgtagta cagcgctgtg catctaataa acctc atg tgc ttg aag atc ctt 893
                                      Met Cys Leu Lys Ile Leu
                                       1   5

gta agg tac aac act agg ggt aat act tat agc act gct tgg ctt tgt 941
Val Arg Tyr Asn Thr Arg Gly Asn Thr Tyr Ser Thr Ala Trp Leu Cys
          10   15   20

gct cta gga aag gtt tta cct ttt cat aga tgg cac act atg gtt caa 989
Ala Leu Gly Lys Val Leu Pro Phe His Arg Trp His Thr Met Val Gln
          25   30   35

aca tgc aca cct aat gtt act atc aac tgt caa gat cca gct ggt ggt 1037
Thr Cys Thr Pro Asn Val Thr Ile Asn Cys Gln Asp Pro Ala Gly Gly
          40   45   50

gcg ctt ata gct agg tgt tgg tac ctt cat gaa ggt cac caa act gct 1085
Ala Leu Ile Ala Arg Cys Trp Tyr Leu His Glu Gly His Gln Thr Ala
55   60   65   70

gca ttt aga gac gta ctt gtt gtt tta aat aaa cga aca aat 1127
Ala Phe Arg Asp Val Leu Val Val Leu Asn Lys Arg Thr Asn
                  75   80

taaaatgtct gataatggac cccaatcaaa ccaacgtagt gcccccgca ttacatttgg 1187
tggacccaca gattcaactg acaataacca gaatggagga cgca 1231

<210> 30
<211> 84
<212> PRT
<213> CORONAVIRUS

<400> 30
Met Cys Leu Lys Ile Leu Val Arg Tyr Asn Thr Arg Gly Asn Thr Tyr
1   5   10   15
Ser Thr Ala Trp Leu Cys Ala Leu Gly Lys Val Leu Pro Phe His Arg
              20   25   30
Trp His Thr Met Val Gln Thr Cys Thr Pro Asn Val Thr Ile Asn Cys
          35   40   45
Gln Asp Pro Ala Gly Gly Ala Leu Ile Ala Arg Cys Trp Tyr Leu His
      50   55   60
Glu Gly His Gln Thr Ala Ala Phe Arg Asp Val Leu Val Val Leu Asn
65   70   75   80
Lys Arg Thr Asn

<210> 31
<211> 21221
<212> DNA
<213> CORONAVIRUS

<400> 31
atggagagcc ttgttcttgg tgtcaacgag aaaacacacg tccaactcag tttgcctgtc 60
cttcaggtta gagacgtgct agtgcgtggc ttcggggact ctgtggaaga ggccctatcg 120
gaggcacgtg aacacctcaa aaatggcact tgtggtctag tagagctgga aaaaggcgta 180
ctgccccagc ttgaacagcc ctatgtgttc attaaacgtt ctgatgcctt aagcaccaat 240
cacggccaca aggtcgttga gctggttgca gaaatggacg gcattcagta cggtcgtagc 300
ggtataacac tggagtactc cgtgccacat gtgggcgaaa ccccaattgc ataccgcaat 360
gttcttcttc gtaagaacgg taataaggga gccggtggtc atagctatgg catcgatcta 420
aagtcttatg acttaggtga cgagcttggc actgatccca ttgaagatta tgaacaaaac 480
tggaacacta agcatggcag tggtgcactc cgtgaactca ctcgtgagct caatggaggt 540
gcagtcactc gctatgtcga caacaatttc tgtggcccag atgggtaccc tcttgattgc 600

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atcaaagatt ttctcgcacg cgcgggcaag tcaatgtgca ctctttccga acaacttgat    660
tacatcgagt cgaagagagg tgtctactgc tgccgtgacc atgagcatga aattgcctgg    720
ttcactgagc gctctgataa gagctacgag caccagacac ccttcgaaat taagagtgcc    780
aagaaatttg acactttcaa aggggaatgc ccaaagtttg tgtttcctct taactcaaaa    840
gtcaaagtca ttcaaccacg tgttgaaaag aaaaagactg agggtttcat ggggcgtata    900
cgctctgtgt accctgttgc atctccacag gagtgtaaca atatgcactt gtctaccttg    960
atgaaatgta atcattgcga tgaagtttca tggcagacgt gcgactttct gaaagccact   1020
tgtgaacatt gtggcactga aaatttagtt attgaaggac ctactacatg tgggtaccta   1080
cctactaatg ctgtagtgaa aatgccatgt cctgcctgtc aagacccaga gattggacct   1140
gagcatagtg ttgcagatta tcacaaccac tcaaacattg aaactcgact ccgcaaggga   1200
ggtaggacta gatgttttgg aggctgtgtg tttgcctatg ttggctgcta taataagcgt   1260
gcctactggg ttcctcgtgc tagtgctgat attggctcag gccatactgg cattactggt   1320
gacaatgtgg agaccttgaa tgaggatctc cttgagatac tgagtcgtga acgtgttaac   1380
attaacattg ttggcgattt tcatttgaat gaagaggttg ccatcatttt ggcatctttc   1440
tctgcttcta caagtgcctt tattgacact ataaagagtc ttgattacaa gtctttcaaa   1500
accattgttg agtcctgcgg taactataaa gttaccaagg gaaagcccgt aaaaggtgct   1560
tggaacattg gacaacagag atcagtttta acaccactgt gtggttttcc ctcacaggct   1620
gctggtgtta tcagatcaat ttttgcgcgc acacttgatg cagcaaacca ctcaattcct   1680
gatttgcaaa gagcagctgt caccatactt gatggtattt ctgaacagtc attacgtctt   1740
gtcgacgcca tggtttatac ttcagacctg ctcaccaaca gtgtcattat tatggcatat   1800
gtaactggtg tcttgtaca acagacttct cagtggttgt ctaatctttt gggcactact   1860
gttgaaaaac tcaggcctat ctttgaatgg attgaggcga aacttagtgc aggagttgaa   1920
tttctcaagg atgcttggga gattctcaaa ttttctcatta caggtgtttt tgacatcgtc   1980
aagggtcaaa tacaggttgc ttcagataac atcaaggatt gtgtaaaatg cttcattgat   2040
gttgttaaca aggcactcga aatgtgcatt gatcaagtca ctatcgctgg cgcaaagttg   2100
cgatcactca acttaggtga agtcttcatc gctcaaagca agggacttta ccgtcagtgt   2160
atacgtggca aggagcagct gcaactactc atgcctctta aggcaccaaa agaagtaacc   2220
tttcttgaag gtgattcaca tgacacagta cttacctctg aggaggttgt tctcaagaac   2280
ggtgaactcg aagcactcga gacgcccgtt gatagcttca caaatggagc tatcgttggc   2340
acaccagtct gtgtaaatgg cctcatgctc ttagagatta aggacaaaga acaatactgc   2400
gcattgtctc ctggtttact ggctacaaac aatgtctttc gcttaaaagg gggtgcacca   2460
attaaaggtg taaccttttgg agaagatact gtttgggaag ttcaaggtta caagaatgtg   2520
agaatcacat ttgagcttga tgaacgtgtt gacaaagtgc ttaatgaaaa gtgctctgtc   2580
tacactgttg aatccggtac cgaagttact gagtttgcat gtgttgtagc agaggctgtt   2640
gtgaagactt tacaaccagt ttctgatctc cttaccaaca tgggtattga tcttgatgag   2700
tggagtgtag ctacattcta cttatttgat gatgctggtg aagaaaactt ttcatcacgt   2760
atgtattgtt cctttttaccc tccagatgag gaagaagagg acgatgcaga gtgtgaggaa   2820
gaagaaattg atgaaacctg tgaacatgag tacggtacag aggatgatta tcaaggtctc   2880
cctctggaat ttggtgcctc agctgaaaca gttcgagttg aggaagaaga gagggaagac   2940
tggctggatg atactactga gcaatcagag attgagccag aaccagaacc tacacctgaa   3000
gaaccagtta atcagtttac tggttatttta aaacttactg acaatgttgc cattaaatgt   3060
gttgacatcg ttaaggaggc acaaagtgct aatcctatgg tgattgtaaa tgctgctaac   3120
atacacctga aacatggtgg tggtgtagca ggtgcactca caaggcaac caatggtgcc   3180
atgcaaaagg agagtgatga ttacattaag ctaaatggcc ctcttacagt aggagggtct   3240
tgtttgcttt ctggacataa tcttgctaag aagtgtctgc atgttgttgg acctaaccta   3300
aatgcaggtg aggacatcca gcttcttaag gcagcatatg aaaatttcaa ttcacaggac   3360
atcttacttg caccattgtt gtcagcaggc atatttggtg ctaaaccact tcagtcttta   3420
caagtgtgcg tgcagacggt tcgtacacag gtttatattg cagtcaatga caaagctctt   3480
tatgagcagg ttgtcatgga ttatcttgat aacctgaagc ctagagtgga agcacctaaa   3540
caagaggagc caccaaacac agaagattcc aaaactgagg agaaatctgt cgtacagaag   3600
cctgtcgatg tgaagccaaa aattaaggcc tgcattgatg aggttaccac aacactggaa   3660
gaaactaagt ttcttaccaa taagttactc ttgtttgctg atatcaatgg taagctttac   3720
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<210> 32
<211> 297
<212> DNA
<213> CORONAVIRUS

<400> 32
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caactgacaa taaccagaat ggaggacgca atggggcaag gccaaaacag cgccgacccc   120
aaggtttacc caataatact gcgtcttggt tcacagctct cactcagcat ggcaaggagg   180
aacttagatt ccctcgaggc cagggcgttc caatcaacac caatagtggt ccagatgacc   240
aaattggcta ctaccgaaga gctacccgac gagttcgtgg tggtgacggc aaaatga   297
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<210> 33
<211> 98
<212> PRT
<213> CORONAVIRUS

<400> 33
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Met Asp Pro Asn Gln Thr Asn Val Val Pro Pro Ala Leu His Leu Val
1               5                   10                  15
Asp Pro Gln Ile Gln Leu Thr Ile Thr Arg Met Glu Asp Ala Met Gly
            20                  25                  30
Gln Gly Gln Asn Ser Ala Asp Pro Lys Val Tyr Pro Ile Ile Leu Arg
        35                  40                  45
Leu Gly Ser Gln Leu Ser Leu Ser Met Ala Arg Arg Asn Leu Asp Ser
    50                  55                  60
Leu Glu Ala Arg Ala Phe Gln Ser Thr Pro Ile Val Val Gln Met Thr
```

```
                     70                  75                    80
Lys Leu Ala Thr Thr Glu Glu Leu Pro Asp Glu Phe Val Val Val Thr
                    85                  90                  95
Ala Lys


<210>   34
<211>   213
<212>   DNA
<213>   CORONAVIRUS

<400>   34
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agggaagcag aggcggcagt caagcctctt ctcgctcctc atcacgtagt cgcggtaatt   120
caagaaattc aactcctggc agcagtaggg gaaattctcc tgctcgaatg gctagcggag   180
gtggtgaaac tgccctcgcg ctattgctgc tag                                213


<210>   35
<211>   70
<212>   PRT
<213>   CORONAVIRUS

<400>   35
Met Leu Pro Pro Cys Tyr Asn Phe Leu Lys Glu Gln His Cys Gln Lys
1                 5                  10                  15
Ala Ser Thr Gln Arg Glu Ala Glu Ala Ala Val Lys Pro Leu Leu Ala
             20                  25                  30
Pro His His Val Val Ala Val Ile Gln Glu Ile Gln Leu Leu Ala Ala
             35                  40                  45
Val Gly Glu Ile Leu Leu Leu Glu Trp Leu Ala Glu Val Val Lys Leu
     50                  55                  60
Pro Ser Arg Tyr Cys Cys
65                  70


<210>   36
<211>   1377
<212>   DNA
<213>   CORONAVIRUS

<220>
<221>   CDS
<222>   (67)..(1335)
<223>

<400>   36
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attaaa atg tct gat aat gga ccc caa tca aac caa cgt agt gcc ccc       108
        Met Ser Asp Asn Gly Pro Gln Ser Asn Gln Arg Ser Ala Pro
        1                 5                   10
cgc att aca ttt ggt gga ccc aca gat tca act gac aat aac cag aat      156
Arg Ile Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn
15                  20                  25                  30
gga gga cgc aat ggg gca agg cca aaa cag cgc cga ccc caa ggt tta      204
Gly Gly Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu
             35                  40                  45
ccc aat aat act gcg tct tgg ttc aca gct ctc act cag cat ggc aag      252
Pro Asn Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys
             50                  55                  60
gag gaa ctt aga ttc cct cga ggc cag ggc gtt cca atc aac acc aat      300
Glu Glu Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn
             65                  70                  75
```

```
agt ggt cca gat gac caa att ggc tac tac cga aga gct acc cga cga    348
Ser Gly Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg
    80                  85                  90

gtt cgt ggt ggt gac ggc aaa atg aaa gag ctc agc ccc aga tgg tac    396
Val Arg Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr
95                 100                 105                 110

ttc tat tac cta gga act ggc cca gaa gct tca ctt ccc tac ggc gct    444
Phe Tyr Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala
            115                 120                 125

aac aaa gaa ggc atc gta tgg gtt gca act gag gga gcc ttg aat aca    492
Asn Lys Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr
            130                 135                 140

ccc aaa gac cac att ggc acc cgc aat cct aat aac aat gct gcc acc    540
Pro Lys Asp His Ile Gly Thr Arg Asn Pro Asn Asn Asn Ala Ala Thr
        145                 150                 155

gtg cta caa ctt cct caa gga aca aca ttg cca aaa ggc ttc tac gca    588
Val Leu Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala
    160                 165                 170

gag gga agc aga ggc ggc agt caa gcc tct tct cgc tcc tca tca cgt    636
Glu Gly Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg
175                 180                 185                 190

agt cgc ggt aat tca aga aat tca act cct ggc agc agt agg gga aat    684
Ser Arg Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn
            195                 200                 205

tct cct gct cga atg gct agc gga ggt ggt gaa act gcc ctc gcg cta    732
Ser Pro Ala Arg Met Ala Ser Gly Gly Gly Glu Thr Ala Leu Ala Leu
            210                 215                 220

ttg ctg cta gac aga ttg aac cag ctt gag agc aaa gtt tct ggt aaa    780
Leu Leu Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys
        225                 230                 235

ggc caa caa caa caa ggc caa act gtc act aag aaa tct gct gct gag    828
Gly Gln Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu
    240                 245                 250

gca tct aaa aag cct cgc caa aaa cgt act gcc aca aaa cag tac aac    876
Ala Ser Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn
255                 260                 265                 270

gtc act caa gca ttt ggg aga cgt ggt cca gaa caa acc caa gga aat    924
Val Thr Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn
            275                 280                 285

ttc ggg gac caa gac cta atc aga caa gga act gat tac aaa cat tgg    972
Phe Gly Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp
            290                 295                 300

ccg caa att gca caa ttt gct cca agt gcc tct gca ttc ttt gga atg   1020
Pro Gln Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met
            305                 310                 315

tca cgc att ggc atg gaa gtc aca cct tcg gga aca tgg ctg act tat   1068
Ser Arg Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr
            320                 325                 330

cat gga gcc att aaa ttg gat gac aaa gat cca caa ttc aaa gac aac   1116
His Gly Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn
335                 340                 345                 350

gtc ata ctg ctg aac aag cac att gac gca tac aaa aca ttc cca cca   1164
Val Ile Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro
            355                 360                 365

aca gag cct aaa aag gac aaa aag aaa aag act gat gaa gct cag cct   1212
Thr Glu Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro
            370                 375                 380

ttg ccg cag aga caa aag aag cag ccc act gtg act ctt ctt cct gcg   1260
Leu Pro Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala
            385                 390                 395
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```
gct gac atg gat gat ttc tcc aga caa ctt caa aat tcc atg agt gga          1308
Ala Asp Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly
    400                     405                 410
gct tct gct gat tca act cag gca taa acactcatga tgaccacaca               1355
Ala Ser Ala Asp Ser Thr Gln Ala
415                     420
aggcagatgg gctatgtaaa cg                                                 1377
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<210> 37
<211> 422
<212> PRT
<213> CORONAVIRUS

<400> 37

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Met Ser Asp Asn Gly Pro Gln Ser Asn Gln Arg Ser Ala Pro Arg Ile
1               5                   10                  15
Thr Phe Gly Gly Pro Thr Asp Ser Thr Asp Asn Asn Gln Asn Gly Gly
            20              25              30
Arg Asn Gly Ala Arg Pro Lys Gln Arg Arg Pro Gln Gly Leu Pro Asn
        35              40              45
Asn Thr Ala Ser Trp Phe Thr Ala Leu Thr Gln His Gly Lys Glu Glu
    50              55              60
Leu Arg Phe Pro Arg Gly Gln Gly Val Pro Ile Asn Thr Asn Ser Gly
65              70              75              80
Pro Asp Asp Gln Ile Gly Tyr Tyr Arg Arg Ala Thr Arg Arg Val Arg
            85              90              95
Gly Gly Asp Gly Lys Met Lys Glu Leu Ser Pro Arg Trp Tyr Phe Tyr
        100             105             110
Tyr Leu Gly Thr Gly Pro Glu Ala Ser Leu Pro Tyr Gly Ala Asn Lys
        115             120             125
Glu Gly Ile Val Trp Val Ala Thr Glu Gly Ala Leu Asn Thr Pro Lys
    130             135             140
Asp His Ile Gly Thr Arg Asn Pro Asn Asn Asn Ala Ala Thr Val Leu
145             150             155             160
Gln Leu Pro Gln Gly Thr Thr Leu Pro Lys Gly Phe Tyr Ala Glu Gly
            165             170             175
Ser Arg Gly Gly Ser Gln Ala Ser Ser Arg Ser Ser Ser Arg Ser Arg
        180             185             190
Gly Asn Ser Arg Asn Ser Thr Pro Gly Ser Ser Arg Gly Asn Ser Pro
    195             200             205
Ala Arg Met Ala Ser Gly Gly Gly Glu Thr Ala Leu Ala Leu Leu Leu
    210             215             220
Leu Asp Arg Leu Asn Gln Leu Glu Ser Lys Val Ser Gly Lys Gly Gln
225             230             235             240
Gln Gln Gln Gly Gln Thr Val Thr Lys Lys Ser Ala Ala Glu Ala Ser
            245             250             255
Lys Lys Pro Arg Gln Lys Arg Thr Ala Thr Lys Gln Tyr Asn Val Thr
        260             265             270
Gln Ala Phe Gly Arg Arg Gly Pro Glu Gln Thr Gln Gly Asn Phe Gly
        275             280             285
Asp Gln Asp Leu Ile Arg Gln Gly Thr Asp Tyr Lys His Trp Pro Gln
290             295             300
Ile Ala Gln Phe Ala Pro Ser Ala Ser Ala Phe Phe Gly Met Ser Arg
305             310             315             320
Ile Gly Met Glu Val Thr Pro Ser Gly Thr Trp Leu Thr Tyr His Gly
            325             330             335
Ala Ile Lys Leu Asp Asp Lys Asp Pro Gln Phe Lys Asp Asn Val Ile
        340             345             350
Leu Leu Asn Lys His Ile Asp Ala Tyr Lys Thr Phe Pro Pro Thr Glu
        355             360             365
Pro Lys Lys Asp Lys Lys Lys Lys Thr Asp Glu Ala Gln Pro Leu Pro
    370             375             380
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Gln Arg Gln Lys Lys Gln Pro Thr Val Thr Leu Leu Pro Ala Ala Asp
385                 390             395                 400
Met Asp Asp Phe Ser Arg Gln Leu Gln Asn Ser Met Ser Gly Ala Ser
                405                 410                 415
Ala Asp Ser Thr Gln Ala
                420
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<210>  38
<211>  1377
<212>  DNA
<213>  CORONAVIRUS

<400>  38
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ggtggaccca cagattcaac tgacaataac cagaatggag gacgcaatgg ggcaaggcca   180
aaacagcgcc gaccccaagg tttacccaat aatactgcgt cttggttcac agctctcact   240
cagcatggca aggaggaact tagattccct cgaggccagg gcgttccaat caacaccaat   300
agtggtccag atgaccaaat tggctactac cgaagagcta cccgacgagt tcgtggtggt   360
gacggcaaaa tgaaagagct cagccccaga tggtacttct attacctagg aactggccca   420
gaagcttcac ttccctacgg cgctaacaaa gaaggcatcg tatgggttgc aactgaggga   480
gccttgaata cacccaaaga ccacattggc acccgcaatc ctaataacaa tgctgccacc   540
gtgctacaac ttcctcaagg aacaacattg ccaaaaggct ctacgcaga gggaagcaga     600
ggcggcagtc aagcctcttc tcgctcctca tcacgtagtc gcggtaattc aagaaattca   660
actcctggca gcagtagggg aaattctcct gctcgaatgg ctagcggagg tggtgaaact   720
gccctcgcgc tattgctgct agacagattg aaccagcttg agagcaaagt ttctggtaaa   780
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ggtccagaac aaacccaagg aaatttcggg gaccaagacc taatcagaca aggaactgat   960
tacaaacatt ggccgcaaat tgcacaattt gctccaagtg cctctgcatt ctttggaatg  1020
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aaattggatg acaaagatcc acaattcaaa gacaacgtca tactgctgaa caagcacatt  1140
gacgcataca aaacattccc accaacagag cctaaaaagg acaaaaagaa aaagactgat  1200
gaagctcagc ctttgccgca gagacaaaag aagcagccca ctgtgactct tcttcctgcg  1260
gctgacatgg atgatttctc cagacaactt caaaattcca tgagtggagc ttctgctgat  1320
tcaactcagg cataaacact catgatgacc acacaaggca gatgggctat gtaaacg     1377

<210>  39
<211>  204
<212>  DNA
<213>  CORONAVIRUS

<400>  39
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ctctaaacga actttaaaat ctgtgtagct gtcgctcggc tgcatgccta gtgcacctac   120
gcagtataaa caataataaa ttttactgtc gttgacaaga aacgagtaac tcgtccctct   180
tctgcagact gcttacggtt tcgt                                          204

<210>  40
<211>  809
<212>  DNA
<213>  CORONAVIRUS

<400>  40
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gcctctgcat ctttggaat gtcacgcatt ggcatggaag tcacaccttc gggaacatgg    180
ctgacttatc atggagccat taaattggat gacaaagatc acaattcaa agacaacgtc     240
atactgctga caagcacat tgacgcatac aaaacattcc caccaacaga gcctaaaaag     300
gacaaaaaga aaaagactga tgaagctcag cctttgccgc agagacaaaa gaagcagccc   360
actgtgactc ttcttcctgc ggctgacatg gatgatttct ccagacaact tcaaaattcc   420
atgagtggag cttctgctga ttcaactcag gcataaacac tcatgatgac cacacaaggc   480
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agatgggcta tgtaaacgtt ttcgcaattc cgtttacgat acatagtcta ctcttgtgca      540
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aatctttaat caatgtgtaa cattagggag gacttgaaag agccaccaca ttttcatcga      660
ggccacgcgg agtacgatcg agggtacagt gaataatgct agggagagct gcctatatgg      720
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<210> 41
<211> 448
<212> DNA
<213> CORONAVIRUS

<400> 41
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aatgaacaca tagggctgtt caagctgggg cagtacgcct ttttccagct ctactagacc       60
acaagtgcca ttttgaggt gttcacgtgc ctccgatagg gcctcttcca cagagtcccc      120
gaagccacgc actagcacgt ctctaacctg aaggacaggc aaactgagtt ggacgtgtgt      180
tttctcgttg acaccaagaa caaggctctc catcttacct ttcggtcaca cccggacgaa      240
acctaggtat gctgatgatc gactgcaaca cggacgaaac cgtaagcagt ctgcagaaga      300
gggacgagtt actcgtttct tgtcaacgac agtaaaattt attattgttt atactgcgta      360
ggtgcactag gcatgcagcc gagcgacagc tacacagatt ttaaagttcg tttagagaac      420
agatctacaa gagatcgagg ttggttgg                                        448
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<210> 42
<211> 2033
<212> DNA
<213> CORONAVIRUS

<400> 42
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tgtgttcatt aaacgttctg atgccttaag caccaatcac ggccacaagg tcgttgagct      300
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gcttggcact gatcccattg aagattatga acaaaactgg aacactaagc atggcagtgg      540
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tctcaaattt ctcattacag gtgtttttga catcgtcaag ggtcaaatac agg           2033
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<210> 43
<211> 2018
<212> DNA
<213> CORONAVIRUS

<400> 43
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ggattgaggc gaaacttagt gcaggagttg aatttctcaa ggatgcttgg gagattctca    60
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acatcaagga ttgtgtaaaa tgcttcattg atgttgttaa caaggcactc gaaatgtgca   180
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tcatgcctct taaggcacca aaagaagtaa cctttcttga aggtgattca catgacacag   360
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ctgtttggga agttcaaggt tacaagaatg tgagaatcac atttgagctt gatgaacgtg   660
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cagttcgagt tgaggaagaa gaagaggaag actggctgga tgatactact gagcaatcag  1080
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ccaaaactga ggagaaatct gtcgtacaga agcctgtcga tgtgaagcca aaaattaagg  1740
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aagatatgtc tttccttgag aaggatgcac cttacatggt aggtgatgtt atcactagtg  1920
gtgatatcac ttgtgttgta ataccctcca aaaaggctgg tggcactact gagatgctct  1980
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<210> 44
<211> 1442
<212> DNA
<213> CORONAVIRUS

<400> 44
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tgtctttcct tgagaaggat gcaccttaca tggtaggtga tgttatcact agtggtgata   180
tcacttgtgt tgtaataccc tccaaaaagg ctggtggcac tactgagatg ctctcaagag   240
ctttgaagaa agtgccagtt gatgagtata taaccacgta ccctggacaa ggatgtgctg   300
gttatacact tgaggaagct aagactgctc ttaagaaatg caaatctgca ttttatgtac   360
taccttcaga agcacctaat gctaaggaag agattctagg aactgtatcc tggaatttga   420
gagaaatgct tgctcatgct gaagagacaa gaaaattaat gcctatgc atggatgtta   480
gagccataat ggcaaccatc caacgtaagt ataaggaat taaaattcaa gagggcatcg   540
ttgactatgg tgtccgattc ttctttata ctagtaaaga gcctgtagct tctattatta   600
cgaagctgaa ctctctaaat gagccgcttg tcacaatgcc aattggttat gtgacacatg   660
gttttaatct tgaagaggct gcgcgctgta tgcgttctct aaagctcct gccgtagtgt   720
cagtatcatc accagatgct gttactacat ataatggata cctcacttcg tcatcaaaga   780
catctgagga gcactttgta gaaacagttt ctttggctgg ctcttacaga gattggtcct   840
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acaacactaa tctccacaca cagcttgtgg atatgtctat gacatatgga cagcagtttg   1080
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gtaagacttt ctttgtacta cctagtgatg acacactacg tagtgaagct ttcgagtact   1200
accatactct tgatgagagt tttcttggta ggtacatgtc tgctttaaac cacacaaaga   1260
aatggaaatt tcctcaagtt ggtggtttaa cttcaattaa atgggctgat aacaattgtt   1320
atttgtctag tgttttatta gcacttcaac agcttgaagt caaattcaat gcaccagcac   1380
ttcaagaggc ttattataga gcccgtgctg gtgatgctgc taacttttgt gcactcatac   1440
tc                                                                   1442
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<210> 45
<211> 1050
<212> DNA
<213> CORONAVIRUS

<400> 45
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atatgtctat gacatatgga cagcagtttg gtccaacata cttggatggt gctgatgtta     60
caaaaattaa acctcatgta aatcatgagg gtaagacttt ctttgtacta cctagtgatg    120
acacactacg tagtgaagct ttcgagtact accatactct tgatgagagt tttcttggta    180
ggtacatgtc tgctttaaac cacacaaaga aatggaaatt tcctcaagtt ggtggtttaa    240
cttcaattaa atgggctgat aacaattgtt atttgtctag tgttttatta gcacttcaac    300
agcttgaagt caaattcaat gcaccagcac ttcaagaggc ttattataga gcccgtgctg    360
gtgatgctgc taacttttgt gcactcatac tcgcttacag taataaaact gttggcgagc    420
ttggtgatgt cagagaaact atgacccatc ttctacagca tgctaatttg gaatctgcaa    480
agcgagttct taatgtggtg tgtaaacatt gtggtcagaa aactactacc ttaacgggtg    540
tagaagctgt gatgtatatg ggtactctat cttatgataa tcttaagaca ggtgtttcca    600
ttccatgtgt gtgtggtcgt gatgctacac aatatctagt acaacaagag tcttcttttg    660
ttatgatgtc tgcaccacct gctgagtata aattacagca aggtacattc ttatgtgcga    720
atgagtacac tggtaactat cagtgtggtc attacactca tataactgct aaggagaccc    780
tctatcgtat tgacggagct caccttacaa agatgtcaga gtacaaagga ccagtgactg    840
atgtttctta caaggaaaca tcttacacta caaccatcaa gcctgtgtcg tataaactcg    900
atggagttac ttacacagag attgaaccaa aattggatgg gtattataaa aaggataatg    960
cttactatac agagcagcct atagaccttg taccaactca accattacca aatgcgagtt   1020
ttgataattt caaactcaca tgttctaaca                                    1050
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<210> 46
<211> 1995
<212> DNA
<213> CORONAVIRUS

<400> 46
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tggtgtgtaa acattgtggt cagaaaacta ctaccttaac gggtgtagaa gctgtgatgt    180
atatgggtac tctatcttat gataatctta agacaggtgt ttccattcca tgtgtgtgtg    240
gtcgtgatgc tacacaatat ctagtacaac aagagtcttc ttttgttatg atgtctgcac    300
cacctgctga gtataaatta cagcaaggta cattcttatg tgcgaatgag tacactggta    360
actatcagtg tggtcattac actcatataa ctgctaagga gaccctctat cgtattgacg    420
gagctcacct tacaaagatg tcagagtaca aaggaccagt gactgatgtt tctacaagg    480
aaacatctta cactacaacc atcaagcctg tgtcgtataa actcgatgga gttacttaca    540
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agcctataga ccttgtacca actcaaccat taccaaatgc gagttttgat aatttcaaac    660
tcacatgttc taacacaaaa tttgctgatg atttaaatca aatgacaggc ttcacaaagc    720
cagcttcacg agagctatct gtcacattct cccagactt gaatggcgat gtagtggcta    780
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aagttgtagg caatgtcata cttaaaccat cagatgaagg tgttaaagta acacaagagt   1140
taggtcatga ggatcttatg gctgcttatg tggaaaacac aagcattacc attaagaaac   1200
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gtttggatgc cggcattaat tatgtgaagt cacccaaatt ttctaaattg ttcacaatcg      1560
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cgatttcatc gtacaagcta gacttgacaa ttttaggtct ggccgctgag tgggtttttgg     1860
catatatgtt gttcacaaaa ttctttatt tattaggtct ttcagctata atgcaggtgt      1920
tctttggcta ttttgctagt catttcatca gcaattcttg gctcatgtgg tttatcatta      1980
gtattgtaca aatgg                                                       1995
```

<210> 47
<211> 1884
<212> DNA
<213> CORONAVIRUS

<400> 47
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aattcttggc tcatgtggtt tatcattagt attgtacaaa tggcacccgt ttctgcaatg      60
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atggatggtt gcacctcttc gacttgcatg atgtgctata agcgcaatcg tgccacacgc      180
gttgagtgta caactattgt taatggcatg aagagatctt ctatgtcta tgcaaatgga      240
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ggtagtacat tcattagtga tgaagttgct cgtgatttgt cactccagtt taaaagacca      360
atcaacccta ctgaccagtc atcgtatatt gttgatagtg ttgctgtgaa aaatggcgcg      420
cttcacctct actttgacaa ggctggtcaa aagacctatg agagacatcc gctctcccat      480
tttgtcaatt tagacaattt gagagctaac aacactaaag gttcactgcc tattaatgtc      540
atagtttttg atggcaagtc caaatgcgac gagtctgctt ctaagtctgc ttctgtgtac      600
tacagtcagc tgatgtgcca acctattctg ttgcttgacc aagctcttgt atcagacgtt      660
ggagatagta ctgaagtttc cgttaagatg tttgatgctt atgtcgacac cttttcagca      720
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gcaaagggtg tagctttaga tggtgtcctt tctacattcg tgtcagctgc ccgacaaggt      840
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atcatacagt ttcctaacac ttacctggag ggttctgtta gagtagtaac aactttgat      1860
gctgagtact gtagacatgg taca                                             1884
```

<210> 48
<211> 2020
<212> DNA
<213> CORONAVIRUS

<400> 48
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cactcgttat gtgcttatgg atggttccat catacagttt cctaacactt acctggaggg      60
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```

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gtcagaagta ggtatttgcc tatctaccag tggtagatgg gttcttaata atgagcatta      180
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<210> 49
<211> 2040
<212> DNA
<213> CORONAVIRUS

<400> 49
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atcattgtgg agttgtacac attgtgccca caatttagaa gatgactcta ctctaagttg     1140
ttgaagaacc gagagcagta ccacagatgt gcactttacg tcagacattt tagactgtac     1200
agtagcaacc ttgatacatg gtttacctcc aatacccaac aacttaatgt taagcttgaa     1260
agcatcaata ctactcttag gaggcaaaag cccctgggag ttcatatacc taaattcttg     1320
tgtagagacc aagtagtcat aaacaccaag agtaagcctg aagtaacggt tgagtaaaca     1380
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gaaaaggcca aagtagcagc agcaacaata gcctaagaaa caataaacaa gcatgataca   1440
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agctctagct aaaaacatga tagtcgtaac gacaccagaa tagttagagg ttacagaaat   1560
aactaaggcc cacatggaaa tagcttgatc taaagcatta ccatagtaga ctttgtaaac   1620
aagtgtaatg acattcatca gtgtccaaac acgtctagca gcatcatcat aaacagtgcg   1680
agctgtcatg agaataagca aaactaaagc tgaagcatac ataacacaat ccttaagcct   1740
ataaccagac aagctagtgt cagccaattc aagccatgtc atgatacgca tcacccagct   1800
agcaggcatg tagaccatat taaagtaagc aactgttgca agagaaggta acagaaacaa   1860
gcacaagaat gcgtgcttat gcttaacaag cagcatagca catgcagcaa ttgccataat   1920
accaagagta aatggcaaga aagcattctc gtaaacaaag aaaaacagtg accactgtgt   1980
actttgaaca agaatcaata gtgatgtcaa gaaagttaaa agcatccaat gatgagtgca   2040
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<211>   2012
<212>   DNA
<213>   CORONAVIRUS
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ttcaggctgg aaatgctaca gaagtacctg ccaattcaac tgtgctttcc ttctgtgctt    180
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ccaactgtgt gaagatgttg tgtacacaca ctggtacagg acaggcaatt actgtaacac    300
cagaagctaa catggaccaa gagtcctttg gtggtgcttc atgttgtctg tattgtagat    360
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gcgtgtacgc caatcattat taaagactgt acaattctgc gatgctatgc gtgatgcagg   1140
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tgactttgct gtgtctaaag gtttctttaa ggaaggaagt tctgttgaac taaaacactt   1860
cttctttgct caggatggca acgctgctat cagtgattat gactattatc gttataatct   1920
gccaacaatg tgtgatatca gacaactcct attcgtagtt gaagttgttg ataaatactt   1980
tgattgttac gatggtggct gtattaatgc ca                                 2012
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<210>   51
<211>   1877
<212>   DNA
<213>   CORONAVIRUS
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cagcattagt ccaatcacat gttgctatcg cattgaagtc agtgacattg tcactgccta    180
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gaggcttatg tgacttgcaa taatagctca tacctcctag atacagttgt gtcacatcag    300
tgacatcaca acctggggca ttgcaaacat agggattaac agacaacact aatttgtgtg    360
atgttgaaat gacatggtca tagcagcact tgcaacatag gaatggtctc ctaatacagg    420
caccgcaacg aagtgaagtc tgtgaattgc acaatacaca agcacctaca gcctgcaaga    480
ctgtatgtgg tgtgtacata gcctcataaa actcaggttc ccagtaccgt gaggtgttat    540
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gcaggtacac gtaatcatct ccttgtttaa ctagcattgt atgctgtgag caaaattcgt    840
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caattaccac agtagctcct ctagtggcgg ctattgactt caataatttc tgatgaaact   1560
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acgcgaaaag tgcatcttga tcctcataac tcattgagtc ataataaagt ctagccttac   1740
cccatttatt aaatgggaaa ccagctgatt tatccagatt gttaacgatt acttggttgg   1800
cattaataca gccaccatcg taacaatcaa agtatttatc aacaacttca actacgaata   1860
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<210> 52
<211> 2051
<212> DNA
<213> CORONAVIRUS

<400> 52
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atacgcacta cattccaggg caagcctta tacatgagtg gtataagatg tttaaactgg    180
tcacctggtg gaggttttgc attaactctg gtgaattctg tgttattttc agtgtcaaca    240
taaccagtcg gtacagctac taagttaaca cctgtagaaa atcctagctg gagaggtagg    300
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cgaacgtgac gaatagcttc ttcgcgggtg ataaacatat tagggtaacc attgacttgg    420
taattcattt tgaaacccat catagagatg agtctacggt aggtcatgtc ctttggtatg    480
cctggtatgt caacacataa tccttcagtc ttgaacttta tatcaacgct gaggtgtgta    540
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actatgcgag cagatgggta atagagagca agtccgatgg caaaatgact cttaccagta   1560
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ccaggtggtc cttggagtgt agagtacttt tgcatgccga ccttttgata atttgcaaca    1620
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tgctcttgtg gcactagagt aggtgcacta agtggcatta cagtgtgaga tgtcaacaca    1740
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tagtcacctt tttcaaaggt gtactctcca atctgtactt tactattttt agttacacgg    1860
taaccagtaa agacatagtt tctgttcaat ggtggtctag gttttccaac ctcccatgaa    1920
agatgcaatt ctctgtcaga gagtacttcg cgtacagtgg caataccata tgacagctta    1980
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<210> 53
<211> 2075
<212> DNA
<213> CORONAVIRUS

<400> 53
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ctttattatc tcgacaaagt catcaagtaa aagatcaatc acagaacaca cacatttga    180
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accgccaagt tgtccatgac tgaaatctcc ataaacgatg tgttcgaagg catagccctc    360
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tgcacgtttg tcacacagac aacacgttct ttcaggtcca atcttgacaa agtacttcat    2040
tgatgtaagc tcaaagccat gcgcccaaag gacga                                2075
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<210> 54
<211> 1891
<212> DNA
<213> CORONAVIRUS

<400> 54
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ttgatgactt tgtcgagata ataaagtcac aagatttgtc agtgatttca aaagtggtca    180
aggttacaat tgactatgct gaaatttcat tcatgctttg gtgtaaggat ggacatgttg    240
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aaaccttcta cccaaaacta caagcaagtc aagcgtggca accaggtgtt gcgatgccta    300
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<210>  56
<211>  32
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<220>
<223>  N antisens primer

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<210>  57
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<212>  DNA
<213>  artificial sequence

<220>
<223>  Sc sens primer

<400>  57
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<212>  DNA
<213>  artificial sequence

<220>
<223>  SL sens primer

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<210>  59
<211>  33
<212>  DNA
<213>  Sc and SL antisens primer

<400>  59
cccccgggtt taatatattg ctcatatttt ccc                                33


<210>  60
<211>  16
<212>  DNA
<213>  Sens set 1 primer

<400>  60
ggcatcgtat gggttg                                                   16


<210>  61
<211>  16
<212>  DNA
<213>  Antisens set 2 (28774-28759) primer

<400>  61
cagtttcacc acctcc                                                   16


<210>  62
<211>  16
<212>  DNA
<213>  Sens set 2 (28375-28390) primer

<400>  62
ggctactacc gaagag                                                   16


<210>  63
<211>  16
<212>  DNA
<213>  Antisens set 2 (28702-28687)primer

<400>  63
aattaccgcg actacg                                                   16


<210>  64
<211>  26
<212>  DNA
<213>  Probe 1/set 1 (28561-28586)

<400>  64
ggcacccgca atcctaataa caatgc                                        26


<210>  65
<211>  21
<212>  DNA
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<213> Probe 2/set 1 (28588-28608)

<400> 65
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<210> 66
<211> 23
<212> DNA
<213> Probe 1/set 2 /probe N/FL (28541-28563)

<400> 66
atacacccaa agaccacatt ggc   23

<210> 67
<211> 25
<212> DNA
<213> Probe 2/set 2/probe SARS/N/LC705 (28565-28589)

<400> 67
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<210> 68
<211> 30
<212> DNA
<213> artificial sequence

<220>
<223> Anchor primer 14T

<400> 68
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<210> 69
<211> 13
<212> PRT
<213> artificial sequence

<220>
<223> M2-14 peptide

<400> 69

Ala Asp Asn Gly Thr Ile Thr Val Glu Glu Leu Lys Gln
1   5   10

<210> 70
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<212> PRT
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<220>
<223> E1-12 peptide

<400> 70
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<210> 71
<211> 24
<212> PRT
<213> artificial sequence

<220>
<223> E53-72 peptide

<400> 71
Lys Pro Thr Val Tyr Val Tyr Ser Arg Val Lys Asn Leu Asn Ser Ser
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Glu Gly Val Pro Asp Leu Leu Val
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<210> 72
<211> 153
<212> DNA
<213> CORONAVIRUS

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cgcagtataa acaataataa attttactgt cgt   153

<210> 73
<211> 410
<212> DNA
<213> CORONAVIRUS

<400> 73
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acactcatga tgaccacaca aggcagatgg gctatgtaaa cgttttcgca attccgttta   120
cgatacatag tctactcttg tgcagaatga attctcgtaa ctaaacagca caagtaggtt   180
tagttaactt taatctcaca tagcaatctt taatcaatgt gtaacattag ggaggacttg   240
aaagagccac cacattttca tcgaggccac gcggagtacg atcgagggta cagtgaataa   300
tgctagggag agctgcctat atggaagagc cctaatgtgt aaaattaatt ttagtagtgc   360
tatccccatg tgattttaat agcttcttag gagaatgaca aaaaaaaaaa   410

<210> 74
<211> 4382
<212> PRT
<213> CORONAVIRUS

<400> 74
Met Glu Ser Leu Val Leu Gly Val Asn Glu Lys Thr His Val Gln Leu
1   5   10   15
Ser Leu Pro Val Leu Gln Val Arg Asp Val Leu Val Arg Gly Phe Gly
            20   25   30
Asp Ser Val Glu Glu Ala Leu Ser Glu Ala Arg Glu His Leu Lys Asn
            35   40   45
Gly Thr Cys Gly Leu Val Glu Leu Glu Lys Gly Val Leu Pro Gln Leu
    50   55   60
Glu Gln Pro Tyr Val Phe Ile Lys Arg Ser Asp Ala Leu Ser Thr Asn
65   70   75   80
His Gly His Lys Val Val Glu Leu Val Ala Glu Met Asp Gly Ile Gln
            85   90   95
Tyr Gly Arg Ser Gly Ile Thr Leu Gly Val Leu Val Pro His Val Gly
            100   105   110
Glu Thr Pro Ile Ala Tyr Arg Asn Val Leu Leu Arg Lys Asn Gly Asn
            115   120   125
Lys Gly Ala Gly Gly His Ser Tyr Gly Ile Asp Leu Lys Ser Tyr Asp
    130   135   140
Leu Gly Asp Glu Leu Gly Thr Asp Pro Ile Glu Asp Tyr Glu Gln Asn
145   150   155   160
Trp Asn Thr Lys His Gly Ser Gly Ala Leu Arg Glu Leu Thr Arg Glu
            165   170   175

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Leu Asn Gly Gly Ala Val Thr Arg Tyr Val Asp Asn Asn Phe Cys Gly
            180                 185                 190
Pro Asp Gly Tyr Pro Leu Asp Cys Ile Lys Asp Phe Leu Ala Arg Ala
            195             200                 205
Gly Lys Ser Met Cys Thr Leu Ser Glu Gln Leu Asp Tyr Ile Glu Ser
    210             215                 220
Lys Arg Gly Val Tyr Cys Cys Arg Asp His Glu His Glu Ile Ala Trp
225             230             235                 240
Phe Thr Glu Arg Ser Asp Lys Ser Tyr Glu His Gln Thr Pro Phe Glu
            245             250                 255
Ile Lys Ser Ala Lys Lys Phe Asp Thr Phe Lys Gly Glu Cys Pro Lys
            260             265                 270
Phe Val Phe Pro Leu Asn Ser Lys Val Lys Val Ile Gln Pro Arg Val
            275             280                 285
Glu Lys Lys Lys Thr Glu Gly Phe Met Gly Arg Ile Arg Ser Val Tyr
    290             295                 300
Pro Val Ala Ser Pro Gln Glu Cys Asn Asn Met His Leu Ser Thr Leu
305             310                 315                 320
Met Lys Cys Asn His Cys Asp Glu Val Ser Trp Gln Thr Cys Asp Phe
            325             330                 335
Leu Lys Ala Thr Cys Glu His Cys Gly Thr Glu Asn Leu Val Ile Glu
            340             345                 350
Gly Pro Thr Thr Cys Gly Tyr Leu Pro Thr Asn Ala Val Val Lys Met
            355             360                 365
Pro Cys Pro Ala Cys Gln Asp Pro Glu Ile Gly Pro Glu His Ser Val
    370             375                 380
Ala Asp Tyr His Asn His Ser Asn Ile Glu Thr Arg Leu Arg Lys Gly
385             390                 395                 400
Gly Arg Thr Arg Cys Phe Gly Gly Cys Val Phe Ala Tyr Val Gly Cys
            405             410                 415
Tyr Asn Lys Arg Ala Tyr Trp Val Pro Arg Ala Ser Ala Asp Ile Gly
            420             425                 430
Ser Gly His Thr Gly Ile Thr Gly Asp Asn Val Glu Thr Leu Asn Glu
            435             440                 445
Asp Leu Leu Glu Ile Leu Ser Arg Glu Arg Val Asn Ile Asn Ile Val
    450             455                 460
Gly Asp Phe His Leu Asn Glu Glu Val Ala Ile Ile Leu Ala Ser Phe
465             470                 475                 480
Ser Ala Ser Thr Ser Ala Phe Ile Asp Thr Ile Lys Ser Leu Asp Tyr
            485             490                 495
Lys Ser Phe Lys Thr Ile Val Glu Ser Cys Gly Asn Tyr Lys Val Thr
            500             505                 510
Lys Gly Lys Pro Val Lys Gly Ala Trp Asn Ile Gly Gln Gln Arg Ser
            515             520                 525
Val Leu Thr Pro Leu Cys Gly Phe Pro Ser Gln Ala Ala Gly Val Ile
    530             535                 540
Arg Ser Ile Phe Ala Arg Thr Leu Asp Ala Ala Asn His Ser Ile Pro
545             550                 555                 560
Asp Leu Gln Arg Ala Ala Val Thr Ile Leu Asp Gly Ile Ser Glu Gln
            565                 570                 575
Ser Leu Arg Leu Val Asp Ala Met Val Tyr Thr Ser Asp Leu Leu Thr
            580                 585                 590
Asn Ser Val Ile Ile Met Ala Tyr Val Thr Gly Gly Leu Val Gln Gln
            595             600                 605
Thr Ser Gln Trp Leu Ser Asn Leu Leu Gly Thr Thr Val Glu Lys Leu
    610             615                 620
Arg Pro Ile Phe Glu Trp Ile Glu Ala Lys Leu Ser Ala Gly Val Glu
625             630                 635                 640
Phe Leu Lys Asp Ala Trp Glu Ile Leu Lys Phe Leu Ile Thr Gly Val
            645                 650                 655
Phe Asp Ile Val Lys Gly Gln Ile Gln Val Ala Ser Asp Asn Ile Lys
            660             665                 670
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Asp Cys Val Lys Cys Phe Ile Asp Val Val Asn Lys Ala Leu Glu Met
        675             680             685
Cys Ile Asp Gln Val Thr Ile Ala Gly Ala Lys Leu Arg Ser Leu Asn
    690             695             700
Leu Gly Glu Val Phe Ile Ala Gln Ser Lys Gly Leu Tyr Arg Gln Cys
705             710             715             720
Ile Arg Gly Lys Glu Gln Leu Gln Leu Leu Met Pro Leu Lys Ala Pro
            725             730             735
Lys Glu Val Thr Phe Leu Glu Gly Asp Ser His Asp Thr Val Leu Thr
            740             745             750
Ser Glu Glu Val Val Leu Lys Asn Gly Glu Leu Glu Ala Leu Glu Thr
            755             760             765
Pro Val Asp Ser Phe Thr Asn Gly Ala Ile Val Gly Thr Pro Val Cys
    770             775             780
Val Asn Gly Leu Met Leu Leu Glu Ile Lys Asp Lys Glu Gln Tyr Cys
785             790             795             800
Ala Leu Ser Pro Gly Leu Leu Ala Thr Asn Asn Val Phe Arg Leu Lys
            805             810             815
Gly Gly Ala Pro Ile Lys Gly Val Thr Phe Gly Glu Asp Thr Val Trp
            820             825             830
Glu Val Gln Gly Tyr Lys Asn Val Arg Ile Thr Phe Glu Leu Asp Glu
            835             840             845
Arg Val Asp Lys Val Leu Asn Glu Lys Cys Ser Val Tyr Thr Val Glu
    850             855             860
Ser Gly Thr Glu Val Thr Glu Phe Ala Cys Val Ala Glu Ala Val
865             870             875             880
Val Lys Thr Leu Gln Pro Val Ser Asp Leu Leu Thr Asn Met Gly Ile
            885             890             895
Asp Leu Asp Glu Trp Ser Val Ala Thr Phe Tyr Leu Phe Asp Asp Ala
            900             905             910
Gly Glu Glu Asn Phe Ser Ser Arg Met Tyr Cys Ser Phe Tyr Pro Pro
            915             920             925
Asp Glu Glu Glu Glu Asp Asp Ala Glu Cys Glu Glu Glu Glu Ile Asp
    930             935             940
Glu Thr Cys Glu His Glu Tyr Gly Thr Glu Asp Asp Tyr Gln Gly Leu
945             950             955             960
Pro Leu Glu Phe Gly Ala Ser Ala Glu Thr Val Arg Val Glu Glu Glu
            965             970             975
Glu Glu Glu Asp Trp Leu Asp Asp Thr Thr Glu Gln Ser Glu Ile Glu
            980             985             990
Pro Glu Pro Glu Pro Thr Pro Glu Glu Pro Val Asn Gln Phe Thr Gly
    995             1000            1005
Tyr Leu Lys Leu Thr Asp Asn Val Ala Ile Lys Cys Val Asp Ile
    1010            1015            1020
Val Lys Glu Ala Gln Ser Ala Asn Pro Met Val Ile Val Asn Ala
    1025            1030            1035
Ala Asn Ile His Leu Lys His Gly Gly Gly Val Ala Gly Ala Leu
    1040            1045            1050
Asn Lys Ala Thr Asn Gly Ala Met Gln Lys Glu Ser Asp Asp Tyr
    1055            1060            1065
Ile Lys Leu Asn Gly Pro Leu Thr Val Gly Gly Ser Cys Leu Leu
    1070            1075            1080
Ser Gly His Asn Leu Ala Lys Lys Cys Leu His Val Val Gly Pro
    1085            1090            1095
Asn Leu Asn Ala Gly Glu Asp Ile Gln Leu Leu Lys Ala Ala Tyr
    1100            1105            1110
Glu Asn Phe Asn Ser Gln Asp Ile Leu Leu Ala Pro Leu Leu Ser
    1115            1120            1125
Ala Gly Ile Phe Gly Ala Lys Pro Leu Gln Ser Leu Gln Val Cys
    1130            1135            1140
Val Gln Thr Val Arg Thr Gln Val Tyr Ile Ala Val Asn Asp Lys
    1145            1150            1155
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Ala Leu Tyr Glu Gln Val Val Met Asp Tyr Leu Asp Asn Leu Lys
    1160                1165                1170
Pro Arg Val Glu Ala Pro Lys Gln Glu Glu Pro Pro Asn Thr Glu
    1175               ·1180                1185
Asp Ser Lys Thr Glu Glu Lys Ser Val Val Gln Lys Pro Val Asp
    1190                1195                1200
Val Lys Pro Lys Ile Lys Ala Cys Ile Asp Glu Val Thr Thr Thr
    1205                1210                1215
Leu Glu Glu Thr Lys Phe Leu Thr Asn Lys Leu Leu Leu Phe Ala
    1220                1225                1230
Asp Ile Asn Gly Lys Leu Tyr His Asp Ser Gln Asn Met Leu Arg
    1235                1240                1245
Gly Glu Asp Met Ser Phe Leu Glu Lys Asp Ala Pro Tyr Met Val
    1250                1255                1260
Gly Asp Val Ile Thr Ser Gly Asp Ile Thr Cys Val Val Ile Pro
    1265                1270                1275  ·
Ser Lys Lys Ala Gly Gly Thr Thr Glu Met Leu Ser Arg Ala Leu
    1280                1285                1290
Lys Lys Val Pro Val Asp Glu Tyr Ile Thr Thr Tyr Pro Gly Gln
    1295                1300                1305
Gly Cys Ala Gly Tyr Thr Leu Glu Glu Ala Lys Thr Ala Leu Lys
    1310                1315                1320
Lys Cys Lys Ser Ala Phe Tyr Val Leu Pro Ser Glu Ala Pro Asn
    1325                1330                1335
Ala Lys Glu Glu Ile Leu Gly Thr Val Ser Trp Asn Leu Arg Glu
    1340                1345                1350
Met Leu Ala His Ala Glu Glu Thr Arg Lys Leu Met Pro Ile Cys
    1355                1360                1365
Met Asp Val Arg Ala Ile Met Ala Thr Ile Gln Arg Lys Tyr Lys
    1370                1375                1380
Gly Ile Lys Ile Gln Glu Gly Ile Val Asp Tyr Gly Val Arg Phe
    1385                1390                1395
Phe Phe Tyr Thr Ser Lys Glu Pro Val Ala Ser Ile Ile Thr Lys
    1400                1405                1410
Leu Asn Ser Leu Asn Glu Pro Leu Val Thr Met Pro Ile Gly Tyr
    1415                1420                1425
Val Thr His Gly Phe Asn Leu Glu Glu Ala Ala Arg Cys Met Arg
    1430                1435                1440
Ser Leu Lys Ala Pro Ala Val Val Ser Val Ser Ser Pro Asp Ala
    1445                1450                1455
Val Thr Thr Tyr Asn Gly Tyr Leu Thr Ser Ser Ser Lys Thr Ser
    1460                1465                1470
Glu Glu His Phe Val Glu Thr Val Ser Leu Ala Gly Ser Tyr Arg
    1475                1480                1485
Asp Trp Ser Tyr Ser Gly Gln Arg Thr Glu Leu Gly Val Glu Phe
    1490                1495                1500
Leu Lys Arg Gly Asp Lys Ile Val Tyr His Thr Leu Glu Ser Pro
    1505                1510                1515
Val Glu Phe His Leu Asp Gly Glu Val Leu Ser Leu Asp Lys Leu
    1520                1525                1530
Lys Ser Leu Leu Ser Leu Arg Glu Val Lys Thr Ile Lys Val Phe
    1535                1540                1545
Thr Thr Val Asp Asn Thr Asn Leu His Thr Gln Leu Val Asp Met
    1550                1555                1560
Ser Met Thr Tyr Gly Gln Gln Phe Gly Pro Thr Tyr Leu Asp Gly
    1565               ·1570                1575
Ala Asp Val Thr Lys Ile Lys Pro His Val Asn His Glu Gly Lys
    1580                1585                1590
Thr Phe Phe Val Leu Pro Ser Asp Asp Thr Leu Arg Ser Glu Ala
    1595                1600                1605
Phe Glu Tyr Tyr His Thr Leu Asp Glu Ser Phe Leu Gly Arg Tyr
    1610                1615                1620
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Met Ser Ala Leu Asn His Thr  Lys Lys Trp Lys Phe  Pro Gln Val
    1625                1630                1635
Gly Gly Leu Thr Ser Ile Lys  Trp Ala Asp Asn Asn  Cys Tyr Leu
    1640                1645                1650
Ser Ser Val Leu Leu Ala Leu  Gln Gln Leu Glu Val  Lys Phe Asn
    1655                1660                1665
Ala Pro Ala Leu Gln Glu Ala  Tyr Tyr Arg Ala Arg  Ala Gly Asp
    1670                1675                1680
Ala Ala Asn Phe Cys Ala Leu  Ile Leu Ala Tyr Ser  Asn Lys Thr
    1685                1690                1695
Val Gly Glu Leu Gly Asp Val  Arg Glu Thr Met Thr  His Leu Leu
    1700                1705                1710
Gln His Ala Asn Leu Glu Ser  Ala Lys Arg Val Leu  Asn Val Val
    1715                1720                1725
Cys Lys His Cys Gly Gln Lys  Thr Thr Thr Leu Thr  Gly Val Glu
    1730                1735                1740
Ala Val Met Tyr Met Gly Thr  Leu Ser Tyr Asp Asn  Leu Lys Thr
    1745                1750                1755
Gly Val Ser Ile Pro Cys Val  Cys Gly Arg Asp Ala  Thr Gln Tyr
    1760                1765                1770
Leu Val Gln Gln Glu Ser Ser  Phe Val Met Met Ser  Ala Pro Pro
    1775                1780                1785
Ala Glu Tyr Lys Leu Gln Gln  Gly Thr Phe Leu Cys  Ala Asn Glu
    1790                1795                1800
Tyr Thr Gly Asn Tyr Gln Cys  Gly His Tyr Thr His  Ile Thr Ala
    1805                1810                1815
Lys Glu Thr Leu Tyr Arg Ile  Asp Gly Ala His Leu  Thr Lys Met
    1820                1825                1830
Ser Glu Tyr Lys Gly Pro Val  Thr Asp Val Phe Tyr  Lys Glu Thr
    1835                1840                1845
Ser Tyr Thr Thr Thr Ile Lys  Pro Val Ser Tyr Lys  Leu Asp Gly
    1850                1855                1860
Val Thr Tyr Thr Glu Ile Glu  Pro Lys Leu Asp Gly  Tyr Tyr Lys
    1865                1870                1875
Lys Asp Asn Ala Tyr Tyr Thr  Glu Gln Pro Ile Asp  Leu Val Pro
    1880                1885                1890
Thr Gln Pro Leu Pro Asn Ala  Ser Phe Asp Asn Phe  Lys Leu Thr
    1895                1900                1905
Cys Ser Asn Thr Lys Phe Ala  Asp Asp Leu Asn Gln  Met Thr Gly
    1910                1915                1920
Phe Thr Lys Pro Ala Ser Arg  Glu Leu Ser Val Thr  Phe Phe Pro
    1925                1930                1935
Asp Leu Asn Gly Asp Val Val  Ala Ile Asp Tyr Arg  His Tyr Ser
    1940                1945                1950
Ala Ser Phe Lys Lys Gly Ala  Lys Leu Leu His Lys  Pro Ile Val
    1955                1960                1965
Trp His Ile Asn Gln Ala Thr  Thr Lys Thr Thr Phe  Lys Pro Asn
    1970                1975                1980
Thr Trp Cys Leu Arg Cys Leu  Trp Ser Thr Lys Pro  Val Asp Thr
    1985                1990                1995
Ser Asn Ser Phe Glu Val Leu  Ala Val Glu Asp Thr  Gln Gly Met
    2000                2005                2010
Asp Asn Leu Ala Cys Glu Ser  Gln Gln Pro Thr Ser  Glu Glu Val
    2015                2020                2025
Val Glu Asn Pro Thr Ile Gln  Lys Glu Val Ile Glu  Cys Asp Val
    2030                2035                2040
Lys Thr Thr Glu Val Val Gly  Asn Val Ile Leu Lys  Pro Ser Asp
    2045                2050                2055
Glu Gly Val Lys Val Thr Gln  Glu Leu Gly His Glu  Asp Leu Met
    2060                2065                2070
Ala Ala Tyr Val Glu Asn Thr  Ser Ile Thr Ile Lys  Lys Pro Asn
    2075                2080                2085
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Glu	Leu 2090	Ser	Leu	Ala	Leu	Gly 2095	Leu	Lys	Thr	Ile	Ala 2100	Thr	His	Gly
Ile	Ala 2105	Ala	Ile	Asn	Ser	Val 2110	Pro	Trp	Ser	Lys	Ile 2115	Leu	Ala	Tyr
Val	Lys 2120	Pro	Phe	Leu	Gly	Gln 2125	Ala	Ala	Ile	Thr	Thr 2130	Ser	Asn	Cys
Ala	Lys 2135	Arg	Leu	Ala	Gln	Arg 2140	Val	Phe	Asn	Asn	Tyr 2145	Met	Pro	Tyr
Val	Phe 2150	Thr	Leu	Leu	Phe	Gln 2155	Leu	Cys	Thr	Phe	Thr 2160	Lys	Ser	Thr
Asn	Ser 2165	Arg	Ile	Arg	Ala	Ser 2170	Leu	Pro	Thr	Thr	Ile 2175	Ala	Lys	Asn
Ser	Val 2180	Lys	Ser	Val	Ala	Lys 2185	Leu	Cys	Leu	Asp	Ala 2190	Gly	Ile	Asn
Tyr	Val 2195	Lys	Ser	Pro	Lys	Phe 2200	Ser	Lys	Leu	Phe	Thr 2205	Ile	Ala	Met
Trp	Leu 2210	Leu	Leu	Leu	Ser	Ile 2215	Cys	Leu	Gly	Ser	Leu 2220	Ile	Cys	Val
Thr	Ala 2225	Ala	Phe	Gly	Val	Leu 2230	Leu	Ser	Asn	Phe	Gly 2235	Ala	Pro	Ser
Tyr	Cys 2240	Asn	Gly	Val	Arg	Glu 2245	Leu	Tyr	Leu	Asn	Ser 2250	Ser	Asn	Val
Thr	Thr 2255	Met	Asp	Phe	Cys	Glu 2260	Gly	Ser	Phe	Pro	Cys 2265	Ser	Ile	Cys
Leu	Ser 2270	Gly	Leu	Asp	Ser	Leu 2275	Asp	Ser	Tyr	Pro	Ala 2280	Leu	Glu	Thr
Ile	Gln 2285	Val	Thr	Ile	Ser	Ser 2290	Tyr	Lys	Leu	Asp	Leu 2295	Thr	Ile	Leu
Gly	Leu 2300	Ala	Ala	Glu	Trp	Val 2305	Leu	Ala	Tyr	Met	Leu 2310	Phe	Thr	Lys
Phe	Phe 2315	Tyr	Leu	Leu	Gly	Leu 2320	Ser	Ala	Ile	Met	Gln 2325	Val	Phe	Phe
Gly	Tyr 2330	Phe	Ala	Ser	His	Phe 2335	Ile	Ser	Asn	Ser	Trp 2340	Leu	Met	Trp
Phe	Ile 2345	Ile	Ser	Ile	Val	Gln 2350	Met	Ala	Pro	Val	Ser 2355	Ala	Met	Val
Arg	Met 2360	Tyr	Ile	Phe	Phe	Ala 2365	Ser	Phe	Tyr	Tyr	Ile 2370	Trp	Lys	Ser
Tyr	Val 2375	His	Ile	Met	Asp	Gly 2380	Cys	Thr	Ser	Ser	Thr 2385	Cys	Met	Met
Cys	Tyr 2390	Lys	Arg	Asn	Arg	Ala 2395	Thr	Arg	Val	Glu	Cys 2400	Thr	Thr	Ile
Val	Asn 2405	Gly	Met	Lys	Arg	Ser 2410	Phe	Tyr	Val	Tyr	Ala 2415	Asn	Gly	Gly
Arg	Gly 2420	Phe	Cys	Lys	Thr	His 2425	Asn	Trp	Asn	Cys	Leu 2430	Asn	Cys	Asp
Thr	Phe 2435	Cys	Thr	Gly	Ser	Thr 2440	Phe	Ile	Ser	Asp	Glu 2445	Val	Ala	Arg
Asp	Leu 2450	Ser	Leu	Gln	Phe	Lys 2455	Arg	Pro	Ile	Asn	Pro 2460	Thr	Asp	Gln
Ser	Ser 2465	Tyr	Ile	Val	Asp	Ser 2470	Val	Ala	Val	Lys	Asn 2475	Gly	Ala	Leu
His	Leu 2480	Tyr	Phe	Asp	Lys	Ala 2485	Gly	Gln	Lys	Thr	Tyr 2490	Glu	Arg	His
Pro	Leu 2495	Ser	His	Phe	Val	Asn 2500	Leu	Asp	Asn	Leu	Arg 2505	Ala	Asn	Asn
Thr	Lys 2510	Gly	Ser	Leu	Pro	Ile 2515	Asn	Val	Ile	Val	Phe 2520	Asp	Gly	Lys
Ser	Lys 2525	Cys	Asp	Glu	Ser	Ala 2530	Ser	Lys	Ser	Ala	Ser 2535	Val	Tyr	Tyr
Ser	Gln 2540	Leu	Met	Cys	Gln	Pro 2545	Ile	Leu	Leu	Leu	Asp 2550	Gln	Ala	Leu

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Val Ser Asp Val Gly Asp Ser   Thr Glu Val Ser Val   Lys Met Phe
    2555            2560                 2565
Asp Ala Tyr Val Asp Thr Phe   Ser Ala Thr Phe Ser   Val Pro Met
    2570            2575                 2580
Glu Lys Leu Lys Ala Leu Val   Ala Thr Ala His Ser   Glu Leu Ala
    2585            2590                 2595
Lys Gly Val Ala Leu Asp Gly   Val Leu Ser Thr Phe   Val Ser Ala
    2600            2605                 2610
Ala Arg Gln Gly Val Val Asp   Thr Asp Val Asp Thr   Lys Asp Val
    2615            2620                 2625
Ile Glu Cys Leu Lys Leu Ser   His His Ser Asp Leu   Glu Val Thr
    2630            2635                 2640
Gly Asp Ser Cys Asn Asn Phe   Met Leu Thr Tyr Asn   Lys Val Glu
    2645            2650                 2655
Asn Met Thr Pro Arg Asp Leu   Gly Ala Cys Ile Asp   Cys Asn Ala
    2660            2665                 2670
Arg His Ile Asn Ala Gln Val   Ala Lys Ser His Asn   Val Ser Leu
    2675            2680                 2685
Ile Trp Asn Val Lys Asp Tyr   Met Ser Leu Ser Glu   Gln Leu Arg
    2690            2695                 2700
Lys Gln Ile Arg Ser Ala Ala   Lys Lys Asn Asn Ile   Pro Phe Arg
    2705            2710                 2715
Leu Thr Cys Ala Thr Thr Arg   Gln Val Val Asn Val   Ile Thr Thr
    2720            2725                 2730
Lys Ile Ser Leu Lys Gly Gly   Lys Ile Val Ser Thr   Cys Phe Lys
    2735            2740                 2745
Leu Met Leu Lys Ala Thr Leu   Leu Cys Val Leu Ala   Ala Leu Val
    2750            2755                 2760
Cys Tyr Ile Val Met Pro Val   His Thr Leu Ser Ile   His Asp Gly
    2765            2770                 2775
Tyr Thr Asn Glu Ile Ile Gly   Tyr Lys Ala Ile Gln   Asp Gly Val
    2780            2785                 2790
Thr Arg Asp Ile Ile Ser Thr   Asp Asp Cys Phe Ala   Asn Lys His
    2795            2800                 2805
Ala Gly Phe Asp Ala Trp Phe   Ser Gln Arg Gly Gly   Ser Tyr Lys
    2810            2815                 2820
Asn Asp Lys Ser Cys Pro Val   Val Ala Ala Ile Ile   Thr Arg Glu
    2825            2830                 2835
Ile Gly Phe Ile Val Pro Gly   Leu Pro Gly Thr Val   Leu Arg Ala
    2840            2845                 2850
Ile Asn Gly Asp Phe Leu His   Phe Leu Pro Arg Val   Phe Ser Ala
    2855            2860                 2865
Val Gly Asn Ile Cys Tyr Thr   Pro Ser Lys Leu Ile   Glu Tyr Ser
    2870            2875                 2880
Asp Phe Ala Thr Ser Ala Cys   Val Leu Ala Ala Glu   Cys Thr Ile
    2885            2890                 2895
Phe Lys Asp Ala Met Gly Lys   Pro Val Pro Tyr Cys   Tyr Asp Thr
    2900            2905                 2910
Asn Leu Leu Glu Gly Ser Ile   Ser Tyr Ser Glu Leu   Arg Pro Asp
    2915            2920                 2925
Thr Arg Tyr Val Leu Met Asp   Gly Ser Ile Ile Gln   Phe Pro Asn
    2930            2935                 2940
Thr Tyr Leu Glu Gly Ser Val   Arg Val Val Thr Thr   Phe Asp Ala
    2945            2950                 2955
Glu Tyr Cys Arg His Gly Thr   Cys Glu Arg Ser Glu   Val Gly Ile
    2960            2965                 2970
Cys Leu Ser Thr Ser Gly Arg   Trp Val Leu Asn Asn   Glu His Tyr
    2975            2980                 2985
Arg Ala Leu Ser Gly Val Phe   Cys Gly Val Asp Ala   Met Asn Leu
    2990            2995                 3000
Ile Ala Asn Ile Phe Thr Pro   Leu Val Gln Pro Val   Gly Ala Leu
    3005            3010                 3015
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Asp Val Ser Ala Ser Val Val Ala Gly Gly Ile Ile Ala Ile Leu
    3020            3025            3030
Val Thr Cys Ala Ala Tyr Tyr Phe Met Lys Phe Arg Arg Val Phe
    3035            3040            3045
Gly Glu Tyr Asn His Val Val Ala Ala Asn Ala Leu Leu Phe Leu
    3050            3055            3060
Met Ser Phe Thr Ile Leu Cys Leu Val Pro Ala Tyr Ser Phe Leu
    3065            3070            3075
Pro Gly Val Tyr Ser Val Phe Tyr Leu Tyr Leu Thr Phe Tyr Phe
    3080            3085            3090
Thr Asn Asp Val Ser Phe Leu Ala His Leu Gln Trp Phe Ala Met
    3095            3100            3105
Phe Ser Pro Ile Val Pro Phe Trp Ile Thr Ala Ile Tyr Val Phe
    3110            3115            3120
Cys Ile Ser Leu Lys His Cys His Trp Phe Phe Asn Asn Tyr Leu
    3125            3130            3135
Arg Lys Arg Val Met Phe Asn Gly Val Thr Phe Ser Thr Phe Glu
    3140            3145            3150
Glu Ala Ala Leu Cys Thr Phe Leu Leu Asn Lys Glu Met Tyr Leu
    3155            3160            3165
Lys Leu Arg Ser Glu Thr Leu Leu Pro Leu Thr Gln Tyr Asn Arg
    3170            3175            3180
Tyr Leu Ala Leu Tyr Asn Lys Tyr Lys Tyr Phe Ser Gly Ala Leu
    3185            3190            3195
Asp Thr Thr Ser Tyr Arg Glu Ala Ala Cys Cys His Leu Ala Lys
    3200            3205            3210
Ala Leu Asn Asp Phe Ser Asn Ser Gly Ala Asp Val Leu Tyr Gln
    3215            3220            3225
Pro Pro Gln Thr Ser Ile Thr Ser Ala Val Leu Gln Ser Gly Phe
    3230            3235            3240
Arg Lys Met Ala Phe Pro Ser Gly Lys Val Glu Gly Cys Met Val
    3245            3250            3255
Gln Val Thr Cys Gly Thr Thr Thr Leu Asn Gly Leu Trp Leu Asp
    3260            3265            3270
Asp Thr Val Tyr Cys Pro Arg His Val Ile Cys Thr Ala Glu Asp
    3275            3280            3285
Met Leu Asn Pro Asn Tyr Glu Asp Leu Leu Ile Arg Lys Ser Asn
    3290            3295            3300
His Ser Phe Leu Val Gln Ala Gly Asn Val Gln Leu Arg Val Ile
    3305            3310            3315
Gly His Ser Met Gln Asn Cys Leu Leu Arg Leu Lys Val Asp Thr
    3320            3325            3330
Ser Asn Pro Lys Thr Pro Lys Tyr Lys Phe Val Arg Ile Gln Pro
    3335            3340            3345
Gly Gln Thr Phe Ser Val Leu Ala Cys Tyr Asn Gly Ser Pro Ser
    3350            3355            3360
Gly Val Tyr Gln Cys Ala Met Arg Pro Asn His Thr Ile Lys Gly
    3365            3370            3375
Ser Phe Leu Asn Gly Ser Cys Gly Ser Val Gly Phe Asn Ile Asp
    3380            3385            3390
Tyr Asp Cys Val Ser Phe Cys Tyr Met His His Met Glu Leu Pro
    3395            3400            3405
Thr Gly Val His Ala Gly Thr Asp Leu Glu Gly Lys Phe Tyr Gly
    3410            3415            3420
Pro Phe Val Asp Arg Gln Thr Ala Gln Ala Ala Gly Thr Asp Thr
    3425            3430            3435
Thr Ile Thr Leu Asn Val Leu Ala Trp Leu Tyr Ala Ala Val Ile
    3440            3445            3450
Asn Gly Asp Arg Trp Phe Leu Asn Arg Phe Thr Thr Thr Leu Asn
    3455            3460            3465
Asp Phe Asn Leu Val Ala Met Lys Tyr Asn Tyr Glu Pro Leu Thr
    3470            3475            3480
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Gln Asp  His Val Asp Ile Leu  Gly Pro Leu Ser Ala  Gln Thr Gly
    3485             3490                 3495
Ile Ala  Val Leu Asp Met Cys  Ala Ala Leu Lys Glu  Leu Leu Gln
    3500             3505                 3510
Asn Gly  Met Asn Gly Arg Thr  Ile Leu Gly Ser Thr  Ile Leu Glu
    3515             3520                 3525
Asp Glu  Phe Thr Pro Phe Asp  Val Val Arg Gln Cys  Ser Gly Val
    3530             3535                 3540
Thr Phe  Gln Gly Lys Phe Lys  Lys Ile Val Lys Gly  Thr His His
    3545             3550                 3555
Trp Met  Leu Leu Thr Phe Leu  Thr Ser Leu Leu Ile  Leu Val Gln
    3560             3565                 3570
Ser Thr  Gln Trp Ser Leu Phe  Phe Phe Val Tyr Glu  Asn Ala Phe
    3575             3580                 3585
Leu Pro  Phe Thr Leu Gly Ile  Met Ala Ile Ala Ala  Cys Ala Met
    3590             3595                 3600
Leu Leu  Val Lys His Lys His  Ala Phe Leu Cys Leu  Phe Leu Leu
    3605             3610                 3615
Pro Ser  Leu Ala Thr Val Ala  Tyr Phe Asn Met Val  Tyr Met Pro
    3620             3625                 3630
Ala Ser  Trp Val Met Arg Ile  Met Thr Trp Leu Glu  Leu Ala Asp
    3635             3640                 3645
Thr Ser  Leu Ser Gly Tyr Arg  Leu Lys Asp Cys Val  Met Tyr Ala
    3650             3655                 3660
Ser Ala  Leu Val Leu Leu Ile  Leu Met Thr Ala Arg  Thr Val Tyr
    3665             3670                 3675
Asp Asp  Ala Ala Arg Arg Val  Trp Thr Leu Met Asn  Val Ile Thr
    3680             3685                 3690
Leu Val  Tyr Lys Val Tyr Tyr  Gly Asn Ala Leu Asp  Gln Ala Ile
    3695             3700                 3705
Ser Met  Trp Ala Leu Val Ile  Ser Val Thr Ser Asn  Tyr Ser Gly
    3710             3715                 3720
Val Val  Thr Thr Ile Met Phe  Leu Ala Arg Ala Ile  Val Phe Val
    3725             3730                 3735
Cys Val  Glu Tyr Tyr Pro Leu  Leu Phe Ile Thr Gly  Asn Thr Leu
    3740             3745                 3750
Gln Cys  Ile Met Leu Val Tyr  Cys Phe Leu Gly Tyr  Cys Cys Cys
    3755             3760                 3765
Cys Tyr  Phe Gly Leu Phe Cys  Leu Leu Asn Arg Tyr  Phe Arg Leu
    3770             3775                 3780
Thr Leu  Gly Val Tyr Asp Tyr  Leu Val Ser Thr Gln  Glu Phe Arg
    3785             3790                 3795
Tyr Met  Asn Ser Gln Gly Leu  Leu Pro Pro Lys Ser  Ser Ile Asp
    3800             3805                 3810
Ala Phe  Lys Leu Asn Ile Lys  Leu Leu Gly Ile Gly  Gly Lys Pro
    3815             3820                 3825
Cys Ile  Lys Val Ala Thr Val  Gln Ser Lys Met Ser  Asp Val Lys
    3830             3835                 3840
Cys Thr  Ser Val Val Leu Leu  Ser Val Leu Gln Gln  Leu Arg Val
    3845             3850                 3855
Glu Ser  Ser Ser Lys Leu Trp  Ala Gln Cys Val Gln  Leu His Asn
    3860             3865                 3870
Asp Ile  Leu Leu Ala Lys Asp  Thr Thr Glu Ala Phe  Glu Lys Met
    3875             3880                 3885
Val Ser  Leu Leu Ser Val Leu  Leu Ser Met Gln Gly  Ala Val Asp
    3890             3895                 3900
Ile Asn  Arg Leu Cys Glu Glu  Met Leu Asp Asn Arg  Ala Thr Leu
    3905             3910                 3915
Gln Ala  Ile Ala Ser Glu Phe  Ser Ser Leu Pro Ser  Tyr Ala Ala
    3920             3925                 3930
Tyr Ala  Thr Ala Gln Glu Ala  Tyr Glu Gln Ala Val  Ala Asn Gly
    3935             3940                 3945
```

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Asp Ser Glu Val Val Leu Lys Lys Leu Lys Lys Ser Leu Asn Val
    3950                3955                3960
Ala Lys Ser Glu Phe Asp Arg Asp Ala Ala Met Gln Arg Lys Leu
    3965                3970                3975
Glu Lys Met Ala Asp Gln Ala Met Thr Gln Met Tyr Lys Gln Ala
    3980                3985                3990
Arg Ser Glu Asp Lys Arg Ala Lys Val Thr Ser Ala Met Gln Thr
    3995                4000                4005
Met Leu Phe Thr Met Leu Arg Lys Leu Asp Asn Asp Ala Leu Asn
    4010                4015                4020
Asn Ile Ile Asn Asn Ala Arg Asp Gly Cys Val Pro Leu Asn Ile
    4025                4030                4035
Ile Pro Leu Thr Thr Ala Ala Lys Leu Met Val Val Val Pro Asp
    4040                4045                4050
Tyr Gly Thr Tyr Lys Asn Thr Cys Asp Gly Asn Thr Phe Thr Tyr
    4055                4060                4065
Ala Ser Ala Leu Trp Glu Ile Gln Gln Val Val Asp Ala Asp Ser
    4070                4075                4080
Lys Ile Val Gln Leu Ser Glu Ile Asn Met Asp Asn Ser Pro Asn
    4085                4090                4095
Leu Ala Trp Pro Leu Ile Val Thr Ala Leu Arg Ala Asn Ser Ala
    4100                4105                4110
Val Lys Leu Gln Asn Asn Glu Leu Ser Pro Val Ala Leu Arg Gln
    4115                4120                4125
Met Ser Cys Ala Ala Gly Thr Thr Gln Thr Ala Cys Thr Asp Asp
    4130                4135                4140
Asn Ala Leu Ala Tyr Tyr Asn Asn Ser Lys Gly Gly Arg Phe Val
    4145                4150                4155
Leu Ala Leu Leu Ser Asp His Gln Asp Leu Lys Trp Ala Arg Phe
    4160                4165                4170
Pro Lys Ser Asp Gly Thr Gly Thr Ile Tyr Thr Glu Leu Glu Pro
    4175                4180                4185
Pro Cys Arg Phe Val Thr Asp Thr Pro Lys Gly Pro Lys Val Lys
    4190                4195                4200
Tyr Leu Tyr Phe Ile Lys Gly Leu Asn Asn Leu Asn Arg Gly Met
    4205                4210                4215
Val Leu Gly Ser Leu Ala Ala Thr Val Arg Leu Gln Ala Gly Asn
    4220                4225                4230
Ala Thr Glu Val Pro Ala Asn Ser Thr Val Leu Ser Phe Cys Ala
    4235                4240                4245
Phe Ala Val Asp Pro Ala Lys Ala Tyr Lys Asp Tyr Leu Ala Ser
    4250                4255                4260
Gly Gly Gln Pro Ile Thr Asn Cys Val Lys Met Leu Cys Thr His
    4265                4270                4275
Thr Gly Thr Gly Gln Ala Ile Thr Val Thr Pro Glu Ala Asn Met
    4280                4285                4290
Asp Gln Glu Ser Phe Gly Gly Ala Ser Cys Cys Leu Tyr Cys Arg
    4295                4300                4305
Cys His Ile Asp His Pro Asn Pro Lys Gly Phe Cys Asp Leu Lys
    4310                4315                4320
Gly Lys Tyr Val Gln Ile Pro Thr Thr Cys Ala Asn Asp Pro Val
    4325                4330                4335
Gly Phe Thr Leu Arg Asn Thr Val Cys Thr Val Cys Gly Met Trp
    4340                4345                4350
Lys Gly Tyr Gly Cys Ser Cys Asp Gln Leu Arg Glu Pro Leu Met
    4355                4360                4365
Gln Ser Ala Asp Ala Ser Thr Phe Leu Asn Gly Phe Ala Val
    4370                4375                4380
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<211> 2695
<212> PRT

<213> CORONAVIRUS

<400> 75

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Thr Ser Thr Asp Val Val Tyr Arg Ala Phe Asp Ile Tyr Asn Glu Lys
            20                  25              30
Val Ala Gly Phe Ala Lys Phe Leu Lys Thr Asn Cys Cys Arg Phe Gln
        35              40              45
Glu Lys Asp Glu Glu Gly Asn Leu Leu Asp Ser Tyr Phe Val Val Lys
    50              55              60
Arg His Thr Met Ser Asn Tyr Gln His Glu Glu Thr Ile Tyr Asn Leu
65              70              75                      80
Val Lys Asp Cys Pro Ala Val Ala Val His Asp Phe Phe Lys Phe Arg
            85              90              95
Val Asp Gly Asp Met Val Pro His Ile Ser Arg Gln Arg Leu Thr Lys
            100             105             110
Tyr Thr Met Ala Asp Leu Val Tyr Ala Leu Arg His Phe Asp Glu Gly
        115             120             125
Asn Cys Asp Thr Leu Lys Glu Ile Leu Val Thr Tyr Asn Cys Cys Asp
    130             135             140
Asp Asp Tyr Phe Asn Lys Lys Asp Trp Tyr Asp Phe Val Glu Asn Pro
145             150             155             160
Asp Ile Leu Arg Val Tyr Ala Asn Leu Gly Glu Arg Val Arg Gln Ser
            165             170             175
Leu Leu Lys Thr Val Gln Phe Cys Asp Ala Met Arg Asp Ala Gly Ile
            180             185             190
Val Gly Val Leu Thr Leu Asp Asn Gln Asp Leu Asn Gly Asn Trp Tyr
            195             200             205
Asp Phe Gly Asp Phe Val Gln Val Ala Pro Gly Cys Gly Val Pro Ile
    210             215             220
Val Asp Ser Tyr Tyr Ser Leu Leu Met Pro Ile Leu Thr Leu Thr Arg
225             230             235             240
Ala Leu Ala Ala Glu Ser His Met Asp Ala Asp Leu Ala Lys Pro Leu
            245             250             255
Ile Lys Trp Asp Leu Leu Lys Tyr Asp Phe Thr Glu Glu Arg Leu Cys
            260             265             270
Leu Phe Asp Arg Tyr Phe Lys Tyr Trp Asp Gln Thr Tyr His Pro Asn
            275             280             285
Cys Ile Asn Cys Leu Asp Asp Arg Cys Ile Leu His Cys Ala Asn Phe
    290             295             300
Asn Val Leu Phe Ser Thr Val Phe Pro Pro Thr Ser Phe Gly Pro Leu
305             310             315             320
Val Arg Lys Ile Phe Val Asp Gly Val Pro Phe Val Val Ser Thr Gly
            325             330             335
Tyr His Phe Arg Glu Leu Gly Val Val His Asn Gln Asp Val Asn Leu
            340             345             350
His Ser Ser Arg Leu Ser Phe Lys Glu Leu Leu Val Tyr Ala Ala Asp
            355             360             365
Pro Ala Met His Ala Ala Ser Gly Asn Leu Leu Leu Asp Lys Arg Thr
    370             375             380
Thr Cys Phe Ser Val Ala Ala Leu Thr Asn Asn Val Ala Phe Gln Thr
385             390             395             400
Val Lys Pro Gly Asn Phe Asn Lys Asp Phe Tyr Asp Phe Ala Val Ser
            405             410             415
Lys Gly Phe Phe Lys Glu Gly Ser Ser Val Glu Leu Lys His Phe Phe
            420             425             430
Phe Ala Gln Asp Gly Asn Ala Ala Ile Ser Asp Tyr Asp Tyr Tyr Arg
            435             440             445
Tyr Asn Leu Pro Thr Met Cys Asp Ile Arg Gln Leu Leu Phe Val Val
450             455             460
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Glu Val Val Asp Lys Tyr Phe Asp Cys Tyr Asp Gly Gly Cys Ile Asn
465   470   475   480

Ala Asn Gln Val Ile Val Asn Asn Leu Asp Lys Ser Ala Gly Phe Pro
            485   490   495

Phe Asn Lys Trp Gly Lys Ala Arg Leu Tyr Tyr Asp Ser Met Ser Tyr
            500   505   510

Glu Asp Gln Asp Ala Leu Phe Ala Tyr Thr Lys Arg Asn Val Ile Pro
    515   520   525

Thr Ile Thr Gln Met Asn Leu Lys Tyr Ala Ile Ser Ala Lys Asn Arg
    530   535   540

Ala Arg Thr Val Ala Gly Val Ser Ile Cys Ser Thr Met Thr Asn Arg
545   550   555   560

Gln Phe His Gln Lys Leu Leu Lys Ser Ile Ala Ala Thr Arg Gly Ala
            565   570   575

Thr Val Val Ile Gly Thr Ser Lys Phe Tyr Gly Gly Trp His Asn Met
            580   585   590

Leu Lys Thr Val Tyr Ser Asp Val Glu Thr Pro His Leu Met Gly Trp
    595   600   605

Asp Tyr Pro Lys Cys Asp Arg Ala Met Pro Asn Met Leu Arg Ile Met
    610   615   620

Ala Ser Leu Val Leu Ala Arg Lys His Asn Thr Cys Cys Asn Leu Ser
625   630   635   640

His Arg Phe Tyr Arg Leu Ala Asn Glu Cys Ala Gln Val Leu Ser Glu
            645   650   655

Met Val Met Cys Gly Gly Ser Leu Tyr Val Lys Pro Gly Gly Thr Ser
            660   665   670

Ser Gly Asp Ala Thr Thr Ala Tyr Ala Asn Ser Val Phe Asn Ile Cys
    675   680   685

Gln Ala Val Thr Ala Asn Val Asn Ala Leu Leu Ser Thr Asp Gly Asn
    690   695   700

Lys Ile Ala Asp Lys Tyr Val Arg Asn Leu Gln His Arg Leu Tyr Glu
705   710   715   720

Cys Leu Tyr Arg Asn Arg Asp Val Asp His Glu Phe Val Asp Glu Phe
            725   730   735

Tyr Ala Tyr Leu Arg Lys His Phe Ser Met Met Ile Leu Ser Asp Asp
            740   745   750

Ala Val Val Cys Tyr Asn Ser Asn Tyr Ala Ala Gln Gly Leu Val Ala
            755   760   765

Ser Ile Lys Asn Phe Lys Ala Val Leu Tyr Tyr Gln Asn Asn Val Phe
    770   775   780

Met Ser Glu Ala Lys Cys Trp Thr Glu Thr Asp Leu Thr Lys Gly Pro
785   790   795   800

His Glu Phe Cys Ser Gln His Thr Met Leu Val Lys Gln Gly Asp Asp
            805   810   815

Tyr Val Tyr Leu Pro Tyr Pro Asp Pro Ser Arg Ile Leu Gly Ala Gly
            820   825   830

Cys Phe Val Asp Asp Ile Val Lys Thr Asp Gly Thr Leu Met Ile Glu
            835   840   845

Arg Phe Val Ser Leu Ala Ile Asp Ala Tyr Pro Leu Thr Lys His Pro
    850   855   860

Asn Gln Glu Tyr Ala Asp Val Phe His Leu Tyr Leu Gln Tyr Ile Arg
865   870   875   880

Lys Leu His Asp Glu Leu Thr Gly His Met Leu Asp Met Tyr Ser Val
            885   890   895

Met Leu Thr Asn Asp Asn Thr Ser Arg Tyr Trp Glu Pro Glu Phe Tyr
            900   905   910

Glu Ala Met Tyr Thr Pro His Thr Val Leu Gln Ala Val Gly Ala Cys
            915   920   925

Val Leu Cys Asn Ser Gln Thr Ser Leu Arg Cys Gly Ala Cys Ile Arg
    930   935   940

Arg Pro Phe Leu Cys Cys Lys Cys Cys Tyr Asp His Val Ile Ser Thr
945   950   955   960

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Ser His Lys Leu Val Leu Ser Val Asn Pro Tyr Val Cys Asn Ala Pro
              965                  970              975
Gly Cys Asp Val Thr Asp Val Thr Gln Leu Tyr Leu Gly Gly Met Ser
              980                  985              990
Tyr Tyr Cys Lys Ser His Lys Pro Pro Ile Ser Phe Pro Leu Cys Ala
          995             1000              1005
Asn Gly Gln Val Phe Gly Leu Tyr Lys Asn Thr Cys Val Gly Ser
    1010             1015             1020
Asp Asn Val Thr Asp Phe Asn Ala Ile Ala Thr Cys Asp Trp Thr
    1025             1030             1035
Asn Ala Gly Asp Tyr Ile Leu Ala Asn Thr Cys Thr Glu Arg Leu
    1040             1045             1050
Lys Leu Phe Ala Ala Glu Thr Leu Lys Ala Thr Glu Glu Thr Phe
    1055             1060             1065
Lys Leu Ser Tyr Gly Ile Ala Thr Val Arg Glu Val Leu Ser Asp
    1070             1075             1080
Arg Glu Leu His Leu Ser Trp Glu Val Gly Lys Pro Arg Pro Pro
    1085             1090             1095
Leu Asn Arg Asn Tyr Val Phe Thr Gly Tyr Arg Val Thr Lys Asn
    1100             1105             1110
Ser Lys Val Gln Ile Gly Glu Tyr Thr Phe Glu Lys Gly Asp Tyr
    1115             1120             1125
Gly Asp Ala Val Val Tyr Arg Gly Thr Thr Thr Tyr Lys Leu Asn
    1130             1135             1140
Val Gly Asp Tyr Phe Val Leu Thr Ser His Thr Val Met Pro Leu
    1145             1150             1155
Ser Ala Pro Thr Leu Val Pro Gln Glu His Tyr Val Arg Ile Thr
    1160             1165             1170
Gly Leu Tyr Pro Thr Leu Asn Ile Ser Asp Glu Phe Ser Ser Asn
    1175             1180             1185
Val Ala Asn Tyr Gln Lys Val Gly Met Gln Lys Tyr Ser Thr Leu
    1190             1195             1200
Gln Gly Pro Pro Gly Thr Gly Lys Ser His Phe Ala Ile Gly Leu
    1205             1210             1215
Ala Leu Tyr Tyr Pro Ser Ala Arg Ile Val Tyr Thr Ala Cys Ser
    1220             1225             1230
His Ala Ala Val Asp Ala Leu Cys Glu Lys Ala Leu Lys Tyr Leu
    1235             1240             1245
Pro Ile Asp Lys Cys Ser Arg Ile Ile Pro Ala Arg Ala Arg Val
    1250             1255             1260
Glu Cys Phe Asp Lys Phe Lys Val Asn Ser Thr Leu Glu Gln Tyr
    1265             1270             1275
Val Phe Cys Thr Val Asn Ala Leu Pro Glu Thr Thr Ala Asp Ile
    1280             1285             1290
Val Val Phe Asp Glu Ile Ser Met Ala Thr Asn Tyr Asp Leu Ser
    1295             1300             1305
Val Val Asn Ala Arg Leu Arg Ala Lys His Tyr Val Tyr Ile Gly
    1310             1315             1320
Asp Pro Ala Gln Leu Pro Ala Pro Arg Thr Leu Leu Thr Lys Gly
    1325             1330             1335
Thr Leu Glu Pro Glu Tyr Phe Asn Ser Val Cys Arg Leu Met Lys
    1340             1345             1350
Thr Ile Gly Pro Asp Met Phe Leu Gly Thr Cys Arg Arg Cys Pro
    1355             1360             1365
Ala Glu Ile Val Asp Thr Val Ser Ala Leu Val Tyr Asp Asn Lys
    1370             1375             1380
Leu Lys Ala His Lys Asp Lys Ser Ala Gln Cys Phe Lys Met Phe
    1385             1390             1395
Tyr Lys Gly Val Ile Thr His Asp Val Ser Ser Ala Ile Asn Arg
    1400             1405             1410
Pro Gln Ile Gly Val Val Arg Glu Phe Leu Thr Arg Asn Pro Ala
    1415             1420             1425
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Trp Arg  Lys Ala Val Phe Ile  Ser Pro Tyr Asn Ser  Gln Asn Ala
    1430             1435             1440
Val Ala  Ser Lys Ile Leu Gly  Leu Pro Thr Gln Thr  Val Asp Ser
    1445             1450             1455
Ser Gln  Gly Ser Glu Tyr Asp  Tyr Val Ile Phe Thr  Gln Thr Thr
    1460             1465             1470
Glu Thr  Ala His Ser Cys Asn  Val Asn Arg Phe Asn  Val Ala Ile
    1475             1480             1485
Thr Arg  Ala Lys Ile Gly Ile  Leu Cys Ile Met Ser  Asp Arg Asp
    1490             1495             1500
Leu Tyr  Asp Lys Leu Gln Phe  Thr Ser Leu Glu Ile  Pro Arg Arg
    1505             1510             1515
Asn Val  Ala Thr Leu Gln Ala  Glu Asn Val Thr Gly  Leu Phe Lys
    1520             1525             1530
Asp Cys  Ser Lys Ile Ile Thr  Gly Leu His Pro Thr  Gln Ala Pro
    1535             1540             1545
Thr His  Leu Ser Val Asp Ile  Lys Phe Lys Thr Glu  Gly Leu Cys
    1550             1555             1560
Val Asp  Ile Pro Gly Ile Pro  Lys Asp Met Thr Tyr  Arg Arg Leu
    1565             1570             1575
Ile Ser  Met Met Gly Phe Lys  Met Asn Tyr Gln Val  Asn Gly Tyr
    1580             1585             1590
Pro Asn  Met Phe Ile Thr Arg  Glu Glu Ala Ile Arg  His Val Arg
    1595             1600             1605
Ala Trp  Ile Gly Phe Asp Val  Glu Gly Cys His Ala  Thr Arg Asp
    1610             1615             1620
Ala Val  Gly Thr Asn Leu Pro  Leu Gln Leu Gly Phe  Ser Thr Gly
    1625             1630             1635
Val Asn  Leu Val Ala Val Pro  Thr Gly Tyr Val Asp  Thr Glu Asn
    1640             1645             1650
Asn Thr  Glu Phe Thr Arg Val  Asn Ala Lys Pro Pro  Pro Gly Asp
    1655             1660             1665
Gln Phe  Lys His Leu Ile Pro  Leu Met Tyr Lys Gly  Leu Pro Trp
    1670             1675             1680
Asn Val  Val Arg Ile Lys Ile  Val Gln Met Leu Ser  Asp Thr Leu
    1685             1690             1695
Lys Gly  Leu Ser Asp Arg Val  Val Phe Val Leu Trp  Ala His Gly
    1700             1705             1710
Phe Glu  Leu Thr Ser Met Lys  Tyr Phe Val Lys Ile  Gly Pro Glu
    1715             1720             1725
Arg Thr  Cys Cys Leu Cys Asp  Lys Arg Ala Thr Cys  Phe Ser Thr
    1730             1735             1740
Ser Ser  Asp Thr Tyr Ala Cys  Trp Asn His Ser Val  Gly Phe Asp
    1745             1750             1755
Tyr Val  Tyr Asn Pro Phe Met  Ile Asp Val Gln Gln  Trp Gly Phe
    1760             1765             1770
Thr Gly  Asn Leu Gln Ser Asn  His Asp Gln His Cys  Gln Val His
    1775             1780             1785
Gly Asn  Ala His Val Ala Ser  Cys Asp Ala Ile Met  Thr Arg Cys
    1790             1795             1800
Leu Ala  Val His Glu Cys Phe  Val Lys Arg Val Asp  Trp Ser Val
    1805             1810             1815
Glu Tyr  Pro Ile Ile Gly Asp  Glu Leu Arg Val Asn  Ser Ala Cys
    1820             1825             1830
Arg Lys  Val Gln His Met Val  Val Lys Ser Ala Leu  Leu Ala Asp
    1835             1840             1845
Lys Phe  Pro Val Leu His Asp  Ile Gly Asn Pro Lys  Ala Ile Lys
    1850             1855             1860
Cys Val  Pro Gln Ala Glu Val  Glu Trp Lys Phe Tyr  Asp Ala Gln
    1865             1870             1875
Pro Cys  Ser Asp Lys Ala Tyr  Lys Ile Glu Glu Leu  Phe Tyr Ser
    1880             1885             1890
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Tyr Ala  Thr His His Asp Lys  Phe Thr Asp Gly Val  Cys Leu Phe
    1895             1900               1905
Trp Asn  Cys Asn Val Asp Arg  Tyr Pro Ala Asn Ala  Ile Val Cys
    1910             1915               1920
Arg Phe  Asp Thr Arg Val Leu  Ser Asn Leu Asn Leu  Pro Gly Cys
    1925             1930               1935
Asp Gly  Gly Ser Leu Tyr Val  Asn Lys His Ala Phe  His Thr Pro
    1940             1945               1950
Ala Phe  Asp Lys Ser Ala Phe  Thr Asn Leu Lys Gln  Leu Pro Phe
    1955             1960               1965
Phe Tyr  Tyr Ser Asp Ser Pro  Cys Glu Ser His Gly  Lys Gln Val
    1970             1975               1980
Val Ser  Asp Ile Asp Tyr Val  Pro Leu Lys Ser Ala  Thr Cys Ile
    1985             1990               1995
Thr Arg  Cys Asn Leu Gly Gly  Ala Val Cys Arg His  His Ala Asn
    2000             2005               2010
Glu Tyr  Arg Gln Tyr Leu Asp  Ala Tyr Asn Met Met  Ile Ser Ala
    2015             2020               2025
Gly Phe  Ser Leu Trp Ile Tyr  Lys Gln Phe Asp Thr  Tyr Asn Leu
    2030             2035               2040
Trp Asn  Thr Phe Thr Arg Leu  Gln Ser Leu Glu Asn  Val Ala Tyr
    2045             2050               2055
Asn Val  Val Asn Lys Gly His  Phe Asp Gly His Ala  Gly Glu Ala
    2060             2065               2070
Pro Val  Ser Ile Ile Asn Asn  Ala Val Tyr Thr Lys  Val Asp Gly
    2075             2080               2085
Ile Asp  Val Glu Ile Phe Glu  Asn Lys Thr Thr Leu  Pro Val Asn
    2090             2095               2100
Val Ala  Phe Glu Leu Trp Ala  Lys Arg Asn Ile Lys  Pro Val Pro
    2105             2110               2115
Glu Ile  Lys Ile Leu Asn Asn  Leu Gly Val Asp Ile  Ala Ala Asn
    2120             2125               2130
Thr Val  Ile Trp Asp Tyr Lys  Arg Glu Ala Pro Ala  His Val Ser
    2135             2140               2145
Thr Ile  Gly Val Cys Thr Met  Thr Asp Ile Ala Lys  Lys Pro Thr
    2150             2155               2160
Glu Ser  Ala Cys Ser Ser Leu  Thr Val Leu Phe Asp  Gly Arg Val
    2165             2170               2175
Glu Gly  Gln Val Asp Leu Phe  Arg Asn Ala Arg Asn  Gly Val Leu
    2180             2185               2190
Ile Thr  Glu Gly Ser Val Lys  Gly Leu Thr Pro Ser  Lys Gly Pro
    2195             2200               2205
Ala Gln  Ala Ser Val Asn Gly  Val Thr Leu Ile Gly  Glu Ser Val
    2210             2215               2220
Lys Thr  Gln Phe Asn Tyr Phe  Lys Lys Val Asp Gly  Ile Ile Gln
    2225             2230               2235
Gln Leu  Pro Glu Thr Tyr Phe  Thr Gln Ser Arg Asp  Leu Glu Asp
    2240             2245               2250
Phe Lys  Pro Arg Ser Gln Met  Glu Thr Asp Phe Leu  Glu Leu Ala
    2255             2260               2265
Met Asp  Glu Phe Ile Gln Arg  Tyr Lys Leu Glu Gly  Tyr Ala Phe
    2270             2275               2280
Glu His  Ile Val Tyr Gly Asp  Phe Ser His Gly Gln  Leu Gly Gly
    2285             2290               2295
Leu His  Leu Met Ile Gly Leu  Ala Lys Arg Ser Gln  Asp Ser Pro
    2300             2305               2310
Leu Lys  Leu Glu Asp Phe Ile  Pro Met Asp Ser Thr  Val Lys Asn
    2315             2320               2325
Tyr Phe  Ile Thr Asp Ala Gln  Thr Gly Ser Ser Lys  Cys Val Cys
    2330             2335               2340
Ser Val  Ile Asp Leu Leu Leu  Asp Asp Phe Val Glu  Ile Ile Lys
    2345             2350               2355
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Ser Gln  Asp Leu Ser Val Ile  Ser Lys Val Val Lys  Val Thr Ile
    2360                 2365                 2370
Asp Tyr  Ala Glu Ile Ser Phe  Met Leu Trp Cys Lys  Asp Gly His
    2375                 2380                 2385
Val Glu  Thr Phe Tyr Pro Lys  Leu Gln Ala Ser Gln  Ala Trp Gln
    2390                 2395                 2400
Pro Gly  Val Ala Met Pro Asn  Leu Tyr Lys Met Gln  Arg Met Leu
    2405                 2410                 2415
Leu Glu  Lys Cys Asp Leu Gln  Asn Tyr Gly Glu Asn  Ala Val Ile
    2420                 2425                 2430
Pro Lys  Gly Ile Met Met Asn  Val Ala Lys Tyr Thr  Gln Leu Cys
    2435                 2440                 2445
Gln Tyr  Leu Asn Thr Leu Thr  Leu Ala Val Pro Tyr  Asn Met Arg
    2450                 2455                 2460
Val Ile  His Phe Gly Ala Gly  Ser Asp Lys Gly Val  Ala Pro Gly
    2465                 2470                 2475
Thr Ala  Val Leu Arg Gln Trp  Leu Pro Thr Gly Thr  Leu Leu Val
    2480                 2485                 2490
Asp Ser  Asp Leu Asn Asp Phe  Val Ser Asp Ala Asp  Ser Thr Leu
    2495                 2500                 2505
Ile Gly  Asp Cys Ala Thr Val  His Thr Ala Asn Lys  Trp Asp Leu
    2510                 2515                 2520
Ile Ile  Ser Asp Met Tyr Asp  Pro Arg Thr Lys His  Val Thr Lys
    2525                 2530                 2535
Glu Asn  Asp Ser Lys Glu Gly  Phe Phe Thr Tyr Leu  Cys Gly Phe
    2540                 2545                 2550
Ile Lys  Gln Lys Leu Ala Leu  Gly Gly Ser Ile Ala  Val Lys Ile
    2555                 2560                 2565
Thr Glu  His Ser Trp Asn Ala  Asp Leu Tyr Lys Leu  Met Gly His
    2570                 2575                 2580
Phe Ser  Trp Trp Thr Ala Phe  Val Thr Asn Val Asn  Ala Ser Ser
    2585                 2590                 2595
Ser Glu  Ala Phe Leu Ile Gly  Ala Asn Tyr Leu Gly  Lys Pro Lys
    2600                 2605                 2610
Glu Gln  Ile Asp Gly Tyr Thr  Met His Ala Asn Tyr  Ile Phe Trp
    2615                 2620                 2625
Arg Asn  Thr Asn Pro Ile Gln  Leu Ser Ser Tyr Ser  Leu Phe Asp
    2630                 2635                 2640
Met Ser  Lys Phe Pro Leu Lys  Leu Arg Gly Thr Ala  Val Met Ser
    2645                 2650                 2655
Leu Lys  Glu Asn Gln Ile Asn  Asp Met Ile Tyr Ser  Leu Leu Glu
    2660                 2665                 2670
Lys Gly  Arg Leu Ile Ile Arg  Glu Asn Asn Arg Val  Val Val Ser
    2675                 2680                 2685
Ser Asp  Ile Leu Val Asn Asn
    2690                 2695
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ccacacacag cttgtggata   20

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ccgaagttgt aggcaatgtc   20

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<210> 138
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